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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:28:36 ; Search time 70 Seconds

(without alignments)
565.363 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRGMGAFVLVLYDEIKKV 297

Scoring table: BLOSUM62

Gapop 10.0 , Capext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

Database :

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1553	100.0	297 21	AAU71031 Human adenine nucl
2	1553	100.0	297 22	AAU01198 Human adenine nucl
3	1553	100.0	297 23	AAU01378 Human adenine nucl
4	1457.5	93.9	298 19	AAU61169 Ant1 protein. Mus
5	1391.5	89.6	298 21	AAU71032 Human adenine nucl
6	1391.5	89.6	298 22	AAU01199 Human adenine nucl
7	1391.5	89.6	298 23	AAU01379 Human adenine nucl
8	1385.5	89.2	298 21	AAU71033 Human polypeptide
9	1385.5	89.2	298 22	AAU39641 Human adenine nucl
10	1385.5	89.2	298 22	AAU01200 Human adenine nucl

11	1385.5	89.2	298	23	AAU10380
12	1385.5	89.2	323	22	AAU41427
13	1294.5	83.4	325	22	ABG15423
14	1241	79.9	299	22	ABG66082
15	1241	79.9	299	22	ABG67300
16	1221.5	78.7	263	22	ABG27056
17	1147	73.9	307	22	ABG58380
18	1101.5	70.9	315	23	ABG21175
19	926.5	59.7	228	23	ABP43205
20	820	52.8	298	22	ABG18922
21	746	48.0	346	21	ACG36577
22	746	48.0	346	21	ACG37261
23	746	48.0	346	21	ACG37264
24	746	48.0	346	21	ACG38460
25	746	48.0	363	21	ACG36576
26	746	48.0	363	21	ACG37260
27	746	48.0	363	21	ACG37263
28	746	48.0	363	21	ACG38459
29	746	48.0	381	21	ACG36575
30	746	48.0	381	21	ACG37259
31	746	48.0	381	21	ACG37252
32	746	48.0	381	21	ACG38458
33	746	48.0	992	21	ACG38672
34	746	48.0	1009	21	ACG38671
35	746	48.0	1027	21	ACG38670
36	743	47.8	346	21	ACG17731
37	743	47.8	363	21	ACG17730
38	743	47.8	381	21	ACG17729
39	734	47.3	386	21	AAU00106
40	724.5	46.7	484	22	ABG15422
41	724.5	46.7	484	22	ABG27055
42	686	44.2	333	21	ACG06857
43	686	44.2	350	21	ACG06856
44	686	44.2	368	21	ACG06855
45	682	43.9	330	21	ACG20658

ALIGNMENTS

RESULT 1
ID AAY71031 standard; Protein: 297 AA.
AC AAY71031:
DT 29-AUG-2000 (first entry)
XX Human adenine nucleotide translocator ANTI.
DE
KW Human: adenine nucleotide translocator: ANTI; mitochondria: ADP: ATP:
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer:
KW mitochondrial permeability transition; neuroprotective; neurotrophic;
KW antiparisonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparisonian; cerbroprotective; therapeutic; Huntington's disease; dystonia;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MEALS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDU;
KW myoclonic epilepsy red ragged fibre syndrome.
XX Homo sapiens.
OS
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1998; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR:
P1 Ghosh SS:
XX WPI: 2000-365619/31.
XX DR N-PSDB: AAD00519.
XX
PT Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
PS Claim 44: Page 172; 175pp; English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator [ANT] from human brain.
XX
SQ Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 21; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVOHASKOISAEKOKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVOHASKOISAEKOKGIIDCVR 60
OY 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
DB 121 GAAGATSLCFYVPLDFARTRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
OY 181 OGIIIRYRAAYFGVYDTAKGMLPDPKNNVHIFVSMIAOSVTAVAGLLSPFTVRRRMNQ 240
DB 181 OGIIIRYRAAYFGVYDTAKGMLPDPKNNVHIFVSMIAOSVTAVAGLLSPFTVRRRMNQ 240
OY 241 SGRKGADIMYGTGVCWKRKIAKDEGAKAFKGCAMSNVLRGMCAGFVLVLYDEIRKVV 297
DB 241 SGRKGADIMYGTGVCWKRKIAKDEGAKAFKGCAMSNVLRGMCAGFVLVLYDEIRKVV 297

RESULT 2
AAU01198
ID AAU01198 standard; Protein: 297 AA.
AC AAU01198;
XX
DT 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-1 (ANT-1) protein.
XX
KW Human: adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX

OS Homo sapiens.
XX
PN WO200132876-A2.
XX
XX 10-MAY-2001.
PD
XX
XX 03-NOV-2000; 2000MO-US30535.
PT
XX
XX 03-NOV-1999; 99US-0434354.
PR
XX
XX (MITO-) MITOKOR.
PA
XX
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
PI Vellicelebi G, Davis RE:
XX
XX WPI: 2001-291054/30.
XX DR N-PSDB: AAS05901.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure: Fig 2; 186pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 22; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVOHASKOISAEKOKGIIDCVR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPLERKLLLOVOHASKOISAEKOKGIIDCVR 60
OY 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
DB 61 IPKEGGLSPFMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRMYPAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
DB 121 GAAGATSLCFYVPLDFARTRLAADVGRRAOREFHGLGDCIIKIFKSDGLRGLYOGFNSV 180
OY 181 OGIIIRYRAAYFGVYDTAKGMLPDPKNNVHIFVSMIAOSVTAVAGLLSPFTVRRRMNQ 240
DB 181 OGIIIRYRAAYFGVYDTAKGMLPDPKNNVHIFVSMIAOSVTAVAGLLSPFTVRRRMNQ 240
OY 241 SGRKGADIMYGTGVCWKRKIAKDEGAKAFKGCAMSNVLRGMCAGFVLVLYDEIRKVV 297
DB 241 SGRKGADIMYGTGVCWKRKIAKDEGAKAFKGCAMSNVLRGMCAGFVLVLYDEIRKVV 297

RESULT 3

AAU10378
ID AAU10378 standard; Protein: 297 AA.
XX
AC AAU10378:
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 1 (ANT1).
XX
KW Human: adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
DR WPI: 2002-055598/07.
DR N-PSDB: AAS16688.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Claim 44: Fig 2: 147pp: English.
XX
CC The invention relates to a recombinant expression construct (1)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (1) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide, ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
SO Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 23; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.2e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 181 OGIIITRAAFGVYDTAKGMLPDKNHHIFVSMHIAOSVTAAGLLSTPPTVRRMMQ 240
OY 241 SGRKADIMYTGTVDCNRKIAKDEGAKAFKGAANSVLKMGCAFVLVLYDEIKKYV 237
DB 241 SGRKADIMYTGTVDCNRKIAKDEGAKAFKGAANSVLKMGCAFVLVLYDEIKKYV 237
RESULT 4
AAW61169
ID AAW61169 standard; Protein: 298 AA.
XX
AC AAW61169;
XX
DT 28-SEP-1998 (first entry)
XX
DE Ant1 protein.
XX
KW Ant1. Adenine nucleotide translocator; cloning; screening;
KW DNA tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
XX
OS Mus sp.
XX
PN WO9819714-A1.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US19882.
XX
PR 01-NOV-1996; 96US-0030017.
XX
PA (UYEM-) UNIV EMORY.
XX
PI Graham BC, Macgregor GR, Wallace DC;
XX
DR WPI: 1998-286608/25.
DR N-PSDB: AAV36479.
XX
PT Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
PS Disclosure: Page 39-40; 61pp: English.
XX
CC The present sequence is the mouse Ant1 protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA
CC Tag diodeoxy terminator cycle sequencing. The Ant1 protein is encoded by
CC the Ant1 locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An Ant1 homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse Ant1 homozygous mutant can be
CC used as a model system for fascioscapular humeral muscular dystrophy,
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of ANT1.
XX
SO Sequence 298 AA:
Query Match 93.9%; Score 1457.5; DB 19; Length 298;
Best Local Similarity 93.6%; Pred. No. 5e-162;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKGLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKGLRGLYOGFNNV 180
 OY 180 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 239
 DB 181 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 240
 OY 240 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGCGAFVLVLYDEIKKYV 297
 DB 241 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGCGAFVLVLYDEIKKYV 298

RESULT 5
 ID AAY71032 standard: Protein: 298 AA.
 AC AAY71032:
 DT 29-AUG-2000 (first entry)
 XX Human adenine nucleotide translocator ANT2.
 DE Human: adenine nucleotide translocator: ANT2; mitochondria: ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; nontoxic; antiParkinsonian; cytostatic; antidiabetic; anticonvulsant; neuroleptic; antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis; Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia; diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS WO200026370-A2.
 PN 11-MAY-2000.
 PD 03-NOV-1999: 99WO-US25883.
 XX 03-NOV-1999: 98US-0185904.
 PR 08-SEP-1999: 99US-0393441.
 XX (MITO-) MITOKOR.
 PA Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR; Ghosh SS.
 PI MPI: 2000-365619/31.
 DR N-PSDB: AAD00520.
 XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX Claim 45: Page 172-173; 175pp: English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d3/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated

CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 XX

SO Sequence 298 AA:
 Query Match 89.6%; Score 1391.5; DB 21; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2,7e-154;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHAWFLKDLFLAGAAVAAVSTAVAPIERVKLLLOVHASKQISAEKQKIDCVNR 60
 DB 1 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 60
 OY 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 DB 61 IPKEGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRIHKOFWRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKGLRGLYOGFNNV 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKGLRGLYOGFNNV 180
 OY 180 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 239
 DB 181 VOGIIRYRAAYFCGYVDTAKGMLPDPKNNVHIFVSMIAQSVTAAGLLSTPFDVRRRRMM 240
 OY 240 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGCGAFVLVLYDEIKKYV 296
 DB 241 OSGRKADIMYTGTVDCMKRIAKDEGAKAFKFGAMSNVLRGCGAFVLVLYDEIKKYV 297

RESULT 6
 ID AAU01199 standard: Protein: 298 AA.
 AC AAU01199:
 DT 07-SEP-2001 (first entry)
 XX Human adenine nucleotide translocator-2 (ANT-2) protein.
 DE Human: adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
 XX mitochondria: ADP; ATP; adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer; mitochondrial permeability transition pore component; cell survival;
 XX mitochondrial core component; mitochondrial related disorder: cancer;
 XX Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 PN 10-MAY-2001.
 PD 03-NOV-2000: 2000WO-US30535.
 XX 03-NOV-2000: 99US-0434354.
 PR 03-NOV-1999: 99US-0434354.
 XX (MITO-) MITOKOR.
 PA Murphy AN, Clevenger W, Willey SE, Andreyev AV, Frigeri LG; Velicelabi G, Davis RE;
 PI MPI: 2001-291054/30.
 DR N-PSDB: AAS05902.
 XX New nucleic acid expression constructs, useful for screening for agents
 XX that alter mitochondrial permeability transition (MPT), comprises
 XX polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 XX fused to energy transfer molecule -

PS Disclosure: Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX
 SO Sequence 298 AA:

Query Match 89.6%; Score 1391.5; DB 22; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.7e-154;
 Matches: 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGKGIIDCVR 60
 DB 1 MTDALSFAPKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOKGIIIDCVR 60

OY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKOLFGLGVDRHKQFMRYFAGNLSAG 120
 DB 61 IPKEEVLSPFRGNLANVIRYPTQALNFAFKDKYKOLFGLGVDRKQFMRYFAGNLSAG 120

OY 121 GAAGATSLCFYYPIDFARTRLAADVGR-AOREFHGSDCIKIFKSGDLGLYOGFNVS 179
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGR-AOREFHGSDCIKIFKSGDLGLYOGFNVS 180

OY 180 VOGIIYRAAFCGYVDTAAGMLPDPKKNHIFVSMIAOSVTAAGLLSYPPDYARRMM 239
 DB 181 VOGIIYRAAFCGYVDTAAGMLPDPKKNHIFVSMIAOTVAVAGLTSYPPDYARRMM 240

OY 240 OSGRKGADIMYTGVDCAWKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGADIMYTGVDCAWKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 297

RESULT 7
 AAU10379
 ID AAU10379 standard; Protein: 298 AA.

XX AAU10379;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX Human adenine nucleotide translocator 2 (ANT2).
 DE
 XX Human: adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200185944-A2.
 XX
 PD 15-NOV-2001.
 XX
 XX 11-MAY-2001; 2001WO-US5416.
 PF
 XX 11-MAY-2000; 2000US-0569327.
 PR
 XX (MITO-) MITOKOR.
 PA

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
 XX
 DR WPI: 2002-055598/07.
 XX N-PSDB; AAS16689.

PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide .

XX
 PS Claim 44: Fig 2; 147pp; English.

XX The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide
 CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide,
 CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human ANT2.

XX
 SO Sequence 298 AA:

Query Match 89.6%; Score 1391.5; DB 23; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.7e-154;
 Matches: 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKYGKGIIDCVR 60
 DB 1 MTDALSFAPKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOKGIIIDCVR 60

OY 61 IPKEGFLSPFRGNLANVIRYPTQALNFAFKDKYKOLFGLGVDRHKQFMRYFAGNLSAG 120
 DB 61 IPKEEVLSPFRGNLANVIRYPTQALNFAFKDKYKOLFGLGVDRKQFMRYFAGNLSAG 120

OY 121 GAAGATSLCFYYPIDFARTRLAADVGR-AOREFHGSDCIKIFKSGDLGLYOGFNVS 179
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGR-AOREFHGSDCIKIFKSGDLGLYOGFNVS 180

OY 180 VOGIIYRAAFCGYVDTAAGMLPDPKKNHIFVSMIAOSVTAAGLLSYPPDYARRMM 239
 DB 181 VOGIIYRAAFCGYVDTAAGMLPDPKKNHIFVSMIAOTVAVAGLTSYPPDYARRMM 240

OY 240 OSGRKGADIMYTGVDCAWKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGADIMYTGVDCAWKIAKDEGAKAFKGAWSNVLRMGCAFVLVLYDEIKKY 297

RESULT 8
 AAAY1033
 ID AAAY1033 standard; Protein: 298 AA.

XX AAAY1033;
 AC
 XX 29-AUG-2000 (first entry)
 DT
 XX Human adenine nucleotide translocator ANT3;
 DE
 XX Human: adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neurotrophic;
 KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;

KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS
 PN WO200026370-A2.
 PD 11-MAY-2000.
 XX
 PF 03-NOV-1999: 99MO-US25883.
 XX
 PR 03-NOV-1998: 98US-0185904.
 PR 08-SEP-1999: 99US-0393441.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
 P1 Ghosh SS.
 DE WPI: 2000-365619/31.
 DE N-PSDB: AAD00521.
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 46, Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC diphosphate across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia.
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 XX
 SQ Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 21; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTTAAPIERVKLLQOVHASKOISAEKQYKIIDCVNR 60
 DB 1 MPEOATISFAKDFLAGGIAAIAAKSTAAPIERVKLLQOVHASKOIAADQYKIVDCIAR 60
 OY 61 IPKEGGLSPMRGNLANVIRYPTQALNFAFKQYKQFLGVDKHTQFRRFAGMLASG 120
 DB 61 IPEOGVLSFMRGNLANVIRYPTQALNFAFKQYKQFLGVDKHTQFRRFAGMLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLADVGR-AOREFHGLGDCIIRFSDGLRGLYQCFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTRLADVGRSGTEREFRLGDCIVVITKSDGLRGLYQCFNVS 180
 OY 180 VOCIITTYRAAYFCVYDTFANGMLPDPKNNVHIFVSWMTAQSVTAVAGLSTPFTDTRRRMM 239
 DB 181 VOCIITTYRAAYFCVYDTFANGMLPDPKNNVHIFVSWMTAQSVTAVAGLSTPFTDTRRRMM 240
 OY 240 OSGRKGADIMYTGTVCWKRINAKDEGAKAFKGCANSNVLRGNGCAFVLVLYDEKKYV 297
 DB 240 OSGRKGADIMYTGTVCWKRINAKDEGAKAFKGCANSNVLRGNGCAFVLVLYDEKKYV 297

DB 241 OSGRKGADIMYTGTVCWKRIFRDEGKAFKGCANSNVLRGNGCAFVLVLYDEKKYV 298

RESULT 9
 ID AAM39641
 XX AAM39641 standard; Protein: 298 AA.
 AC
 XX AAM39641:
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 2786.
 XX
 XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KM peripheral nervous system; neuropathy; central nervous system; CNS;
 KM Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KM amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM leukaemia.
 XX
 OS Homo sapiens.
 OS
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000MO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AA158797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries
 XX
 PS Example 4: SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM39642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: immune system suppression,
 CC Actin/Inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC C.N.S disorders,
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 22; Length 298;
 Best Local Similarity 87.2%; Pred. No. 1.4e-153;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

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QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60
DB 1 MTEQAIISFAKDFLAGIAAIAISKTAVAPIERVKLLLOVHASKOIAADKQYKGIYDCIVR 60
QY 61 IPKEGFLSPFMRGNLANVIRYPTQALNFAFDKXKQFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGFLSPFMRGNLANVIRYPTQALNFAFDKXKQFLGVDNRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 179
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 180
QY 180 VOGIIYRAAFGVYDTAKGMLPDPKNTHIVVSMIAQVTAVAGLVSPPTVRRMM 239
DB 180 VOGIIYRAAFGVYDTAKGMLPDPKNTHIVVSMIAQVTAVAGLVSPPTVRRMM 239
QY 240 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 297
DB 240 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 297
QY 241 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 298
DB 241 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 298

RESULT 10
AAU01200
ID AAU01200 standard: Protein: 298 AA.
XX
AC AAU01200:
XX
DT 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-3 (ANT-3) protein.
XX
KW Human: adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
PN WO200132876-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000: 2000MO-US30535.
XX
PR 03-NOV-1999: 990S-0434354.
XX
PA (MITO-) MITOKOR.
XX
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Vellicelebi G, Davis RE;
XX
DR MPI: 2001-291054/30.
XX
DR N-PSDB: AAS05903.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule.
XX
PS Disclosure: Fig 2, 186pp: English.
XX
CC The present sequence represents human adenine nucleotide translocator-3
CC (ANT-3) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability

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CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA:
XX
Query Match 89.2%; Score 1385.5; DB 22; Length 298;
Best Local Similarity 87.2%; Pred. No. 1.4e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1:

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60
DB 1 MTEQAIISFAKDFLAGIAAIAISKTAVAPIERVKLLLOVHASKOIAADKQYKGIYDCIVR 60
QY 61 IPKEGFLSPFMRGNLANVIRYPTQALNFAFDKXKQFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGFLSPFMRGNLANVIRYPTQALNFAFDKXKQFLGVDNRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 179
QY 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-AOREFHGLDCIIKIFKSDGLRGLYOGFNV 180
QY 180 VOGIIYRAAFGVYDTAKGMLPDPKNTHIVVSMIAQVTAVAGLVSPPTVRRMM 239
DB 180 VOGIIYRAAFGVYDTAKGMLPDPKNTHIVVSMIAQVTAVAGLVSPPTVRRMM 239
QY 240 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 297
DB 240 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 297
QY 241 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 298
DB 241 OSGRKGADIMYGTGDCWKRKIAKDEGAKAFFGAMSNVLRGCGAFVLVLYDEIKKYV 298

RESULT 11
AAU10380
ID AAU10380 standard: Protein: 298 AA.
XX
AC AAU10380:
XX
DT 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 3 (ANT3).
XX
KW Human: adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001: 2001MO-US15416.
XX
PR 11-MAY-2000: 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pel Y, Carroll AK;
XX
DR MPI: 2002-055598/07.
XX
DR N-PSDB: AAS16690.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
PS Example 3; Fig 2; 147pp: English.
XX

```

CC The invention relates to a recombinant expression construct (1)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (1) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT3.
XX
S0 Sequence 298 AA:

Query Match 89.2%: Score 1385.5; DB 23; Length 298;
Best Local Similarity 87.2%: Pred. No. 1.4e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHWSFLKDFLAGAANAASKTVAPIERVKLLLOVHASKOISAEKOYKGIIDCVNR 60
DB 1 MTEQALSFADFLAGGIAAIAISKTVAPIERVKLLLOVHASKOIAADKOYKGIIDCVNR 60
OY 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKKYKOLFLGVDRIHQFRRYFAGNLASG 120
DB 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKKYKOLFLGVDRIHQFRRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIFKSDGLRGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIFKSDGLRGLYOGFNVS 180
OY 180 VGGIITIRAAVFCGYVDPAKGMPLDPKRVHIFVSMIAOSTAVAGLLSYFDDTVRRRM 239
DB 181 VGGIITIRAAVFCGYVDPAKGMPLDPKRVHIFVSMIAOSTAVAGLLSYFDDTVRRRM 240
OY 240 QSGRKADIMYGTCTVDCMKRKADEGAKAFKGAWSNVLRGMCAPVLLVYDEIKKYV 297
DB 241 QSGRKADIMYGTCTVDCMKRKADEGAKAFKGAWSNVLRGMCAPVLLVYDEIKKYV 298

RESULT 12

AAM41427 standard; Protein: 323 AA.

XX ID AAM41427:
XX AC AAM41427:
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 6358.
XX OS Homo sapiens.
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000MO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XD, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX

DR WPI: 2001-442253/47.

DR N-PSDB: AAI60383.

PT Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -

PS Example 2: SEQ ID NO 6358; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

S0 Sequence 323 AA:

Query Match 89.2%: Score 1385.5; DB 22; Length 323;
Best Local Similarity 87.2%: Pred. No. 1.6e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHWSFLKDFLAGAANAASKTVAPIERVKLLLOVHASKOISAEKOYKGIIDCVNR 60
DB 26 MTEQALSFADFLAGGIAAIAISKTVAPIERVKLLLOVHASKOIAADKOYKGIIDCVNR 85
OY 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKKYKOLFLGVDRIHQFRRYFAGNLASG 120
DB 61 IPKEGFLSFMRGNLANVIRYPTQALNFAFKKYKOLFLGVDRIHQFRRYFAGNLASG 145
OY 86 IPKEGFLSFMRGNLANVIRYPTQALNFAFKKYKOLFLGVDRIHQFRRYFAGNLASG 179
DB 121 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIFKSDGLRGLYOGFNVS 205
OY 146 GAAGATSLCFVYPLDPAFRTLRADVGR-AOREFHGIGDCIIFKSDGLRGLYOGFNVS 239
DB 180 VGGIITIRAAVFCGYVDPAKGMPLDPKRVHIFVSMIAOSTAVAGLLSYFDDTVRRRM 265
OY 206 VGGIITIRAAVFCGYVDPAKGMPLDPKRVHIFVSMIAOSTAVAGLLSYFDDTVRRRM 297
DB 240 QSGRKADIMYGTCTVDCMKRKADEGAKAFKGAWSNVLRGMCAPVLLVYDEIKKYV 323
OY 266 QSGRKADIMYGTCTVDCMKRKADEGAKAFKGAWSNVLRGMCAPVLLVYDEIKKYV 323

RESULT 13

ABG15423 standard; Protein: 325 AA.

XX ID ABG15423:
XX AC ABG15423:
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #15414.

XX	Human: Chromosome mapping; gene mapping; gene therapy; forensic;
KM	food supplement; medical imaging; diagnostic; genetic disorder.
OS	Ilomo sapiens.
PN	MO2001.75067-A2.
XX	11-OCT-2001.
XX	30-MAR-2001; 2001WO-US08631.
PP	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HYSED INC.
PA	Drimanac RT, Liu C, Tang YT;
P1	WPI: 2001-639362/73.
XX	N-PSDB; AAS79610.
DR	New isolated polynucleotide and encoded polypeptides, useful in
XX	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	Claim 20; SEQ ID No 45782; 103pp; English.
PS	The invention relates to isolated polynucleotide (I) and
CC	polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC	polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC	and gene mapping, and in recombinant production of (II). The
CC	polynucleotides are also used in diagnostics as expressed sequence tags
CC	for identifying expressed genes. (I) is useful in gene therapy techniques
CC	to restore normal activity of (II) or to treat disease states involving
CC	(II). (II) is useful for generating antibodies against it, detecting or
CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. ABG00010-ABG30377 represent novel human
CC	diagnostic amino acid sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
XX	Sequence 325 AA:
XX	Query Match 83.4%; Score 1294.5; DB 22; Length 325;
XX	Best Local Similarity 83.4%; Pred. No. 7.3e-143;
XX	Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4
OY	1 MGHANSLKDFLAGAANAASKTVAPRIERYKLLDYOVHASKOISAEKQYKIDCVNR 60
DB	24 MTDAAVSFAKDFLAGAANAASKTVAPRIERYKLLDYOVHASKOIAADKQYKIDCVNR 83
OY	61 IPKEGGFLSPFMGNLANVIRFPPOLANFAFDKKYKQLFGVDGRHKQRMRYRAGNLAS 120
DB	84 IPKEGGVLSFMGRGNLANVIRFPPOLANFAFDKKYKQLFGVDGRKQRMRYRANRLAS 143
OY	121 GAAGATSLCFVYPLDFAFTRLAADYGR-AOREFNLGDCIIKIEKSDSLRGLYOGFNVS 179
DB	144 GAAGATSLCFVYPLDFAFTRLAADYGR-AOREFNLGDCIIKIEKSDSLRGLYOGFNVS 203
OY	180 VOGIITRYAAAFGVYDTAKGMLPDRKNNHIFVSWMIAGSV-TAAVAGLSTYPTT--VRRR 236
DB	204 VOGIITRYAAAFGVYDTAKGMLPDRKNNHIFVSWMIAGSV-TAAVAGLSTYPTT--VRRR 263

Oy		237	MAMOSGRGADIMYGTATDCWRKIACKDEGAKAFPGAMSNTVLRMGCAFVLVD-EIKR	295
D6		264	EXMOSRGKTDMYTGLTDCWKIARDECAGAKFPKGAMSNLVRGMCGAVLVLEYEKSKK	323
Oy		296 Y 296 324 Y 324		
D8				
		RESULT 14		
		ID ABB66082		
Xx		ABB66082 standard; Protein: 299 AA.		
Xx				
AC		ABBE6082;		
Xx				
DT		26-MAR-2002 (first entry)		
Xx				
DE		Drosophila melanogaster polypeptide SEQ ID NO 25038.		
Xx				
KW		Drosophil; developmental biology; cell signalling; insecticide; pharmaceutical.		
Xx				
OS		Drosophila melanogaster.		
Xx				
PN		WO200171042-A2.		
Xx				
PD		27-SEP-2001.		
Xx				
PE		23-MAR-2001; 2001WO-US09231.		
Xx				
PR		23-MAR-2000; 2000US-191637P. 11-JUL-2000; 2000US-061415O.		
Xx				
PA		(PERE) PE CORP NY.		
Xx				
PI		Venter JC, Adams M, Li PWD, Myers EW:		
DR		WP1: 2001-656860/75.		
N-PSDB: ABLL0185.				
XX		New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -		
PT				
PS		Disclosure: SEQ ID NO 25038; 21pp + Sequence Listing; English.		
Cc		The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLJ6176-ABLJ3051), expressed DNA sequences (ABLJ01840-ABLJ6175) and the encoded proteins (ABBS7737-ABBJ2072).		
Cc		The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.		
S0		Sequence 299 AA:		
Oy	Query Match	79.9%; Score 1241; DB 22; Length 299;		
	Best Local Similarity	79.7%; Pred. No. 1.2e-136;		
	Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0			
D6		5 AMSFLKDPLACAAVAASRTNAVAPLERVKLLLOVNHASKSIOIAERQYKKIIIDCVNPRIKE 64 : : :: :		
Oy		7 AVGFVKDDAAGCISAASKVSTNAVIPERKLLLVOYHSKOISDPDYOKCMVCDFIRIPKE 66 : : :: :		
D6		OGFSLFSEGNLANIVRYPPTOALNFAPFDKYKQLFGIGVDRIKHOFMRYPAGNLASGGANG 124 :		
Oy		67 OGSSFMNGNLANIVRYIPTOLANFAPFDKYKQYLGVGDKNITOTFRMYRPNAGNLASGGANG 126 :		
Oy		125 ATSLCEVVPLDFARTLADVGRAOREFHGIICDI IKIFKSDBGRLGLGYGFNVSVQG II 184		

Db 127 ATSLCEPVYPLDFARFLRLAADTGKGGGRETGTGNCUTKIFPSDGIYGLYRFGVSYGII 166

Oy 185 IYPAATFCYVDTAKGKLPPKXVHIFVSMIAQSTAVAGLSTPFDTVRRRRMMOSGRK 244

Db 187 IYRAAFYGFYDTRGRLPDPKNTPIYISMAIQVYTTAAGIVSYSPFDVRRRRMMOSGRK 246

Oy 245 GAIIMYGTVCDCWRKIAKDEGAFFKPKGMSVVLGMSGAPVLVYDEIKK 295

Db 247 ATEVYIKNTLHCMAITAKOEGTGAFKPKAFNSILNGTGAFVLYLYDEIKK 297

RESULT 15
ABB67300
ID ABB67300 standard; Protein; 299 AA.

AC ABB67300;

DT 26-MAR-2002 (first entry)

Drosophila melanogaster polypeptide SEQ ID NO 28692.

KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmacological.
KW

Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P

XX
DA / DEVE) DE CORR WIRXX
DTXX
DB
UNIT: 2001-666060.7E

DR N-PSDB; ABL11403.
XY

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from *Drosophila* and for elucidating cell signalling and cell-cell-
PT interactions -

PS Disclosure; SEQ ID NO 28692; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from *Drosophila*. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB161617-AB163051), expressed DNA
CC sequences (AB101840-AB161615) and the encoded proteins
CC (AB557737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at [ftp.wipo.int/pub/published_pcc_sequences](http://wipo.int/pub/published_pcc_sequences).

SQ Sequence 299 AA;

Query Match	79.98;	Score 1241;	DB 22;	Length 299;
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Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;

QY 5 AWSFLKDFLAGAVAAVSKTAVAPIERVKLLLOVQHASKQISAEKQYKGIIDCVVRIPKE 64

Db 7 AVGFVKDFAAGISAAVSKTAVAPIERVKLLQVQHISKQISPDKQYKGMVDCFIRIPKE 66

65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYQQLFCGVDHRKHQFWRYFAGNLASGGAG 124

Db 6 QGFSFMRGNLANVIRYPTQALNFAFDKTKYVFLGGVDKNTQFMWRIFAGNLASGGAAG 126

Oy 125 ATSLCFVYPLDPAARTRLAADVGRAROREFHGLGDCI K1FKSDGLRGLYGCFNVSVOCII 184

Db 127 ATSLCFVYPLDPAARTRLAADTGCGRRETFGLGNC LTK1FKSDGIWGLYKCFVSVOCII 186

Oy 185 IYAAAFVGYDPAKGLDPKKNVH1FVSM1AQSVTAAGLSYPPDVRBRMMOSGRK 244

Db 187 IYAAAFGEYDPAKGLDPKKNTPIY1SM1AQQVTVAGIVSYPPDVRBRMMOSGRK 246

Oy 245 GABIMYTGVDVCDRIAKDECAKAFPFKASNVILGMGCAVLVLYDEIK 295

Db 247 ATEVITKNTLHCMTIAKQEGTCGAFPKAFSNIILRGTCGAVLVLYDEIK 297

Search completed: June 18, 2003, 13:34:03
Job time : 71 secs

Job time : 71 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Fun on: June 18, 2003, 13:20:01 ; Search time 15 Seconds

(Without alignments)
562.574 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHANSFLKDFLAGAVAA.....LRGNGAFVLVDEIKKY 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1457.5	93.9	298	3	US-08-961-871-10 Sequence 10, Appl
2	301	19.4	469	4	US-09-188-930-339 Sequence 339, App
3	291	18.7	447	4	US-09-160-119-4 Sequence 4, Appl
4	291	18.7	674	4	US-09-160-119-2 Sequence 2, Appl
5	267	17.2	291	4	US-09-501-558-2 Sequence 2, Appl
6	238	15.3	320	2	US-08-933-750C-12 Sequence 12, Appl
7	238	15.3	320	4	US-09-234-613-12 Sequence 12, Appl
8	233.5	15.0	312	4	US-09-142-565-2 Sequence 2, Appl
9	227	14.6	299	1	US-08-518-878B-56 Sequence 56, Appl
10	227	14.6	299	2	US-08-470-868A-56 Sequence 56, Appl
11	227	14.6	309	1	US-08-518-878B-51 Sequence 51, Appl
12	227	14.6	309	2	US-08-807-861A-51 Sequence 51, Appl
13	227	14.6	309	2	US-08-470-868A-51 Sequence 51, Appl
14	227	14.6	309	3	US-09-210-681-51 Sequence 51, Appl
15	227	14.6	309	3	US-08-946-719A-51 Sequence 51, Appl
16	227	14.6	311	2	US-08-775-009-33 Sequence 33, Appl
17	225	14.5	311	2	US-08-775-009-32 Sequence 32, Appl
18	222.5	14.3	308	2	US-08-937-466-2 Sequence 2, Appl
19	222.5	14.3	308	2	US-09-172-528-2 Sequence 2, Appl
20	222.5	14.3	308	4	US-09-318-199-2 Sequence 2, Appl
21	222.5	14.3	308	4	US-09-503-579-2 Sequence 2, Appl
22	218.5	14.1	432	2	US-08-937-466-4 Sequence 4, Appl
23	218.5	14.1	432	2	US-09-172-528-4 Sequence 4, Appl
24	218.5	14.1	432	3	US-09-318-199-4 Sequence 4, Appl
25	218.5	14.1	432	4	US-09-503-579-4 Sequence 4, Appl
26	208.5	13.4	293	4	US-09-501-558-4 Sequence 4, Appl
27	196.5	12.7	307	2	US-08-807-861A-56 Sequence 56, Appl

28	196.5	12.7	307	3	US-09-210-681-56 Sequence 56, Appl
29	196.5	12.7	307	3	US-08-946-719A-56 Sequence 56, Appl
30	193	12.4	303	1	US-08-294-522B-36 Sequence 36, Appl
31	192	12.4	303	1	US-08-518-878B-37 Sequence 37, Appl
32	192	12.4	303	2	US-08-807-861A-37 Sequence 37, Appl
33	192	12.4	303	2	US-08-470-868A-37 Sequence 37, Appl
34	192	12.4	303	3	US-09-210-681-37 Sequence 37, Appl
35	192	12.4	303	3	US-08-946-719A-37 Sequence 37, Appl
36	190.5	12.3	306	5	PCT-US94-09799-1 Sequence 1, Appl
37	188.5	12.1	351	2	US-08-933-750C-19 Sequence 19, Appl
38	188.5	12.1	351	4	US-09-234-613-19 Sequence 15, Appl
39	185.5	11.9	328	4	US-09-068-140A-15 Sequence 6, Appl
40	176	11.3	256	2	US-08-937-466-6 Sequence 6, Appl
41	176	11.3	256	2	US-09-172-528-6 Sequence 6, Appl
42	176	11.3	256	3	US-09-318-199-6 Sequence 6, Appl
43	176	11.3	256	4	US-09-503-579-6 Sequence 6, Appl
44	176	11.3	312	4	US-09-188-930-142 Sequence 142, App
45	175.5	11.3	289	4	US-09-068-140A-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: MacGregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
NUMBER OF INVENTION: Nucleotide Translocator Protein and Methods
CORRESPONDENCE ADDRESS: 11
ADDRESS: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%, Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 4,1e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
OY 1 MGDHANSFLKDFLAGAVAAVSKTRAVPIERVKLLLOVQASKQISAEKQYKGIIDCVR 60

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DB 1 MDDQALSLFKDPLAGIAAASKTAVPIERVKLLLOVQHASKOISAEKQYGIIDCVR 60
OY 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKOFWRYPAGNLASG 120
DB 61 IPKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKOFWRYPAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTTAAADVKGSSOREFNGDCLTKIRKSDGLKGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTTAAADVKGSSOREFNGDCLTKIRKSDGLKGLYOGFSVS 180
OY 180 VGGIIRYRAVFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLSPPTVRRRMH 239
DB 180 VGGIIRYRAVFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLSPPTVRRRMH 239
OY 240 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGSANVLRGSGAFVLVYDEIKYV 297
DB 240 OSGRGADIMYTGTVDCMRKIAKDEGAKAFKGSANVLRGSGAFVLVYDEIKYV 297
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RESULT 2
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PRT
ORGANISM: Mouse
US-09-188-930-339

Query Match 19.4% Score 301; DB 4; Length 469;
Best Local Similarity 28.9%; Pred. No. 2, 4e-26;
Matches 89; Conservative 64; Mismatches 103; Indels 52; Gaps 14;

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OY 6 WSFLKDFLAGAVAAVSKTAVPIERVKLLLOVQHASKOISAEKQYGIIDCVR---RI 61
DB 187 WRLH---VAGGGAGAVSRCTAPLDRKLVLMQV-HASRSNM-----CLVGGFTOM 233
OY 62 PKEGGLFSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGCVDR---HKOFWRYPAGN 116
DB 234 IREGAKSLWRGNGINVLKIAPEISAKFMAVEQMKRLV---GSDQETLRHIER----- 283
OY 117 LASGGAATSLCFVYPLDFARTTAAADVKGSSOREFNGDCLTKIRKSDGLKGLYOGF 176
DB 284 LVAGSLAGIAOSSIYPMEVLTAKTRMAL---RKTGYSGMLDCARRILAKEGVAAAFYKG 339
OY 177 NVSVGGIIRYRAVFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLSPPTVRRRMH 239
DB 340 IPMMLGIIIPYAGIDLAVETLKTMTLQRTAVNSADP---GVFY-LIACGISTTCOLAS 395
OY 228 YPDDTVARRMMOSGRRGADIMYTGTVDCMRKIAKDEGAKAFKGSANVLRGSGAFV- 286
DB 396 YPLAVTRTRMQAOASIEGAPEVTMSL--FKQILRTGAGAGLVRLAPNFMKVIYPAVSIS 453
OY 287 LVLYDEIK 294
DB 454 YVYVENLK 461
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RESULT 3

```
US-09-160-119-4
Sequence 4, Application US/09160119A
Patent No. 6316219
GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRILL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT FILING DATE: 1998-09-24
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 447
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-4
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Query Match 18.7% Score 291; DB 4; Length 447;
Best Local Similarity 27.5%; Pred. No. 3, 2e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

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OY 12 FLAGAVAAVSKTAVPIERVKLLLOVQHASKOISAEKQYGIIDCVRIIPKEGGLFSW 71
DB 104 FGLGSVAGAVGATVAVPIDLVTRHONQSTGFSVGLYKNSFDCKFVLRKEGFGLY 163
OY 72 RGNLANVIRYPTQALNFAFKDKYKQLFLGCVDRHKOFWRYPAGNLASGAGATSLCFV 131
DB 164 RGLLPDLGVAPPEAKKLTVDNPFVRKFM---HNDGSVPLAELIAGCAGGSOVIFT 218
OY 132 YPLDFARTL--AADV--GRRAROREFHGDCIIRKFSKSDGLKGLYOGFNVSVGGI 187
DB 219 NPLEIVKIRLOVAGETTTGPRVS-----ALSVVRDLGFFGIYKKAACFLRBIIPS 269
OY 188 AAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAV-AGLSTPFDTVARRMMOSGRKGA 246
DB 270 AIFYPCYAHVHKASFANEDQVSPCSILLAGAIAGMPASLVTPADVIKTR--LOVVARAG 327
OY 247 DIMYTGTVDCMRKIAKDEGAKAFKGSANVLRGSGAFVLVYDEIKY 296
DB 328 QTTYSGVIDCFRILREBGRKALMGAGARVFRSSPQFGVTLTYELLDRW 378
```

RESULT 4
US-09-160-119-2
Sequence 2, Application US/09160119A
Patent No. 6316219

GENERAL INFORMATION:
APPLICANT: KRIEF, STEPHANE
APPLICANT: SOUCHET, MICHEL
APPLICANT: BRILL, ANTOINE
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GH-30985
CURRENT FILING DATE: 1998-09-24
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1997-10-23
EARLIER FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 674
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-160-119-2

Query Match 18.7% Score 291; DB 4; Length 674;

[illegible]

```

RESULT 5
US-09-501-558-2
Sequence 2, Application US/09501558
Patent No. 6403784
GENERAL INFORMATION:
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Mathur, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. 6403784el Human Uncoupling Proteins and
FILE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: Lex-0012-USA
CURRENT APPLICATION NUMBER: US/09/501,558
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Homo sapiens
US-09-501-558-2

```

Query Match 17.2%; Score 267; DB 4; Length 291;
Best Local Similarity 28.4%; Pred. No. 1e-22;
Matches 84; Conservative 51; Mismatches 137; Indels 24; Gaps 9;

RESULT 6
US-08-933-750C-12

Sequence 12: Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933.750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLNNOT02
CLONE: 207452
US-08-933-750C-12

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Query Match 15 38: Score 238: DB 2: Length 320:
      Similarity 23.58: Pred. No. 2.8e-19:
Matches 71: Conservative 67: Mismatches 124: Indels 40: Gaps 10:

Oy 13 LAGAVAAVASKTAAPIERVKLLLYOVNHAS-KQISAKQYKGIIDCVARIPEKQGLSPW 71
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 20 VAGSVGSLVTALLSPFDVIKIRQDOLHERLSRSDPSAKNGLIOLASROTLQEGSPAFW 79
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Oy 72 RGNLANVYRYFFPTQALNF-AFKDKYKOLFSGVDNRHKQMYRFAGNLSAGAAATSLCF 130
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 80 KGHVPAQILSTIGYAVQOFLSPFEMLTVELNHRSGVYDAREFSVNF-----VCGSLAACMATLT 135
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Oy 131 VYPLDFAFTRILAADVGRAPROREFGLGDCIIKIFKSGSLGVLQVGFNVSVOGIITYAAAY 190
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 136 VHPDVLTARTPEFA---QSEPKVYUPTTLRHAAGTMYRSEGGPOVFYKGLPTALIAFPVAGLQ 192
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Oy 191 FGVDVDTAKGMLPDKKNHIFVSMNI-----AQSVAAGLSTVFPDFTVAR 235
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Db 193 FSCYSSSLK-----HLY-KWAI PAEGCKNEMLOLLCGSGGAGVY SKTTLTPPLDLFFK 242
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Oy 236 RMMN---QSGRK--GADIMYTGTVDCNRKIATKDEGAAPFGAWSNLNR-GMGCAFVYL 289
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

```


REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-470-868A-51

Query Match 14.6% Score 227; DB 2; Length 309;
Best Local Similarity 23.8% Pred. NO. 5e-18;

Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

DB 12 FLAGVANAASVTNAPIERVKLLLOVQHASK---QISAEKQYKGIIDCVIRIPKEGFL 68
17 FLAGACTAACIADLITFPIDTAKVRLIOGESOGPVKATVSAQYKGMGTILTMVTEGPR 76
CY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDYDRHKQFWRYPAGNLASGAGATSL 128
DB 77 SLVNGLVAGLOROMSFASVRIGLYDSVKOFYTKGEHNS-----IGSRLASTGTALAV 131
CY 129 CFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSDGLGLYOGFNVSOGIITIRA 188
DB 132 AVAOPTDVVKVFFQARAGCGRRYOSTVNAYKTIAREGCFGLMKGTSPNARNAIVNC 191
CY 189 AVFGYVDTRAK-----GMLPDKNNHIFVSMHIAOSYAVACLLSPEDTVRRMMOSG 242
DB 192 AELVYTDLIKDALLANLMTDLPCH-FTSAFGAGCTTV---IASPDVVVTRTM---- 243
CY 243 RKGADIMYTGVDWCRKIAKDEGAKAFKFGAMSNVLR-GMGCAFVLYLDEIK 295
DB 244 -NSALGQYSSAGHCALTMLOKCGPRAFYKGFMPSTLRIGSNMNVVFVTEQLKR 296

RESULT 14

US-09-210-681-51
Sequence 51, Application US/09210681
Patent No. 6057109

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITILE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-09-210-681-51

Query Match 14.6% Score 227; DB 3; Length 309;
Best Local Similarity 23.8% Pred. NO. 5e-18;

Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

DB 12 FLAGVANAASVTNAPIERVKLLLOVQHASK---QISAEKQYKGIIDCVIRIPKEGFL 68
17 FLAGACTAACIADLITFPIDTAKVRLIOGESOGPVKATVSAQYKGMGTILTMVTEGPR 76
CY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDYDRHKQFWRYPAGNLASGAGATSL 128
DB 77 SLVNGLVAGLOROMSFASVRIGLYDSVKOFYTKGEHNS-----IGSRLASTGTALAV 131
CY 129 CFVYPLDFARTRLADVGRRAOREFHGLDCLIKIFKSDGLGLYOGFNVSOGIITIRA 188
DB 132 AVAOPTDVVKVFFQARAGCGRRYOSTVNAYKTIAREGCFGLMKGTSPNARNAIVNC 191
CY 189 AVFGYVDTRAK-----GMLPDKNNHIFVSMHIAOSYAVACLLSPEDTVRRMMOSG 242
DB 192 AELVYTDLIKDALLANLMTDLPCH-FTSAFGAGCTTV---IASPDVVVTRTM---- 243
CY 243 RKGADIMYTGVDWCRKIAKDEGAKAFKFGAMSNVLR-GMGCAFVLYLDEIK 295
DB 244 -NSALGQYSSAGHCALTMLOKCGPRAFYKGFMPSTLRIGSNMNVVFVTEQLKR 296

RESULT 15

US-08-946-719A-51
Sequence 51, Application US/08946719A
Patent No. 6121017

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITILE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,719A
FILING DATE: 8-OCT-1997
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995

APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-107
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-946-719A-51

Query Match 14.6% Score 227; DB 3; Length 309;
Best Local Similarity 23.8% Pred. No. 5e-18;
Matches 70; Conservative 52; Mismatches 148; Indels 24; Gaps 7;

OY 12 FLAGAVAAAVSKTAVAPIERYKLLLOVHASK---QISAEROYKGIIDCVVRIPEEGFL 68
D0 17 FLAGGTACIADLTFTPLDTAKVRLIQGESQCPVRAVSAQYRGVWGTTLTWVTEGPR 76
OY 69 SFARGNLANVIRFPTQALNFAFDKYKQLFLGCVDRHKOFWRYFAGNLASGGAAGATSL 128
D0 77 SLVNGLVAGLOROMSPASVRIGLYDSVKOFYTKGSEHAS----IGSRLLAGSTTGALAV 131
OY 129 CFVYPLDFARTRLADYGRAROREFHGLGDCIIKIFKSDGLRGLYOGFNVSGIITYRA 188
D0 132 AVAOPTDVVKRFQARAGGGRRYOSTVNAVYKTIAREEGFRGLMKGTSPVARNAIYVC 191
OY 189 AYFCVYDTAK-----GMLPDPKNVHIFVSMIAOSYTAAGLSYPPDVRRRMMQSG 242
D0 192 AELVYDULIKDALKANLMTDDLPCH--FTSAFGAGFCTTV---IASPVDVVKTRYM----- 243
OY 243 RKGADIMYTGVCWRKIAKDEGAKAFKGAWSNVLK-GMGAFVLVLYDEIKK 295
D0 244 -NSALCOYSSAGICALTJLQKEGPRAFYKCFMPSFLRLGSMNVVMFVTEQLKR 296

Search completed: June 18, 2003, 13:28:53
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:27:41 : Search time 23 Seconds
(without alignments)
1397.279 Million cell updates/sec

Title: US-09-393-441-31
Perfect score: 1553

Sequence: 1 MGDHWSFLKDFLAGAFAA.....LRMGCAFVLVDLKKYV 297

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 417779 seqs, 108206813 residues

Total number of hits satisfying chosen parameters: 417779

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB pep:.*
14: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1553	100.0	297	US-09-185-904A-31	Sequence 31, App1
2	1553	100.0	297	US-09-811-094-31	Sequence 31, App1
3	1553	100.0	297	US-09-810-644-31	Sequence 31, App1
4	1391.5	89.6	298	US-09-185-904A-32	Sequence 32, App1
5	1391.5	89.6	298	US-09-811-094-32	Sequence 32, App1
6	1391.5	89.6	298	US-09-810-644-32	Sequence 32, App1
7	1385.5	89.2	298	US-09-185-904A-33	Sequence 33, App1
8	1385.5	89.2	298	US-09-811-094-33	Sequence 33, App1
9	1385.5	89.2	298	US-09-810-644-33	Sequence 33, App1
10	734	47.3	318	US-09-801-368-252	Sequence 252, App
11	734	47.3	318	US-09-734-569-170	Sequence 170, App
12	461	29.7	132	US-09-925-501-1459	Sequence 1459, App
13	461	29.7	132	US-09-864-761-36440	Sequence 36440, A
14	350.5	22.6	475	US-09-777-921A-4	Sequence 4, App11
15	346.5	22.3	477	US-09-777-921A-2	Sequence 2, App11
16	312	20.1	410	US-09-777-921A-5	Sequence 5, App11
17	304	19.6	469	US-09-992-588-289	Sequence 289, App
18	304	19.6	469	US-09-989-293A-289	Sequence 289, App
19	304	19.6	469	US-10-063-547-58	Sequence 58, App1

ALIGNMENTS

RESULT 1
US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wile, Sandra Elleen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAY
FILE REFERENCE: 660088.420
CURRENT FILING DATE: 1998-11-03
CURRENT APPLICATION NUMBER: US/09/185, 904A
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRP
ORGANISM: Homo sapien
US-09-185-904A-31
Query Match 100.0%; Score 1553; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 2e-157;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 61 MGDHWSFLKDFLAGAFAA...SKTAVPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60
1 IPRKQGLTFMRGRLAVIRYFPFOALNPAFKDKYKOLFLGGVDRHOFKPFYFAGNLASG 120
61 IPRKQGLTFMRGRLAVIRYFPFOALNPAFKDKYKOLFLGGVDRHOFKPFYFAGNLASG 120
Db 61 IPRKQGLTFMRGRLAVIRYFPFOALNPAFKDKYKOLFLGGVDRHOFKPFYFAGNLASG 120
121 GAAGCATSLCFYPLDFARTRLAADVGRRAOREFHGLDCJIIKIFKSDGLNGLYOGFNVSV 180
121 GAAGCATSLCFYPLDFARTRLAADVGRRAOREFHGLDCJIIKIFKSDGLNGLYOGFNVSV 180

OY 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
DB 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
OY 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297

RESULT 2

US-09-811-094-31

Sequence 31, Application US/09811094

Patent No. US20010044144A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Moos, Walter H.

APPLICANT: Pel, Yashong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D4

CURRENT APPLICATION NUMBER: US/09/811.094

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

US-09-811-094-31

Query Match 100.0%; Score 1553; DB 10; Length 297;

Best Local Similarity 100.0%; Pred. No. 2e-157;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVRR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVRR 60
OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGDCGCIKIFKSDGLRGLYGFNSV 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGDCGCIKIFKSDGLRGLYGFNSV 180
OY 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
DB 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
OY 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297

RESULT 3

US-09-810-644-31

Sequence 31, Application US/09810644

Patent No. US20020012992A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Moos, Walter H.

APPLICANT: Pel, Yashong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D3

CURRENT APPLICATION NUMBER: US/09/810.644

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 31

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

US-09-810-644-31

Query Match 100.0%; Score 1553; DB 10; Length 297;

Best Local Similarity 100.0%; Pred. No. 2e-157;

Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVRR 60
DB 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVRR 60
OY 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEGGLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGDCGCIKIFKSDGLRGLYGFNSV 180
DB 121 GAAGATSLCFVYPLDFAFTRRLAADVGRRAOREFHGDCGCIKIFKSDGLRGLYGFNSV 180
OY 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
DB 181 OGIIYRAAYFGVYDTAKGMLPDPKNVHI FVSMIAOSVTAVAGLLSTPPTVRRMMQ 240
OY 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297
DB 241 SGRKADIMYGTGTCVDCMKRIAKDEGAKAFFGGAMSNTLRGAGAFVLVLYDEIKKYV 297

RESULT 4

US-09-185-904A-32

Sequence 32, Application US/09185904A

Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAY

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185.904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 32

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;

Best Local Similarity 88.6%; Pred. No. 3.4e-140;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEOYKGIIDCVRR 60
DB 1 MTDAAALSTAKDFLAGAANAASKTAVAPIERVKLLQVOHASKOITADKOYKGIIDCVRR 60


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OY      61  PKEEGPFSEFMGNLANIYIRFPQALNFAFDKXKOLFLEGVDBDHQWRRFAGNLAAG  120
Db      61  IPKEDEVLSFMGNLANIIRFPQALNFAFDKXKOLFLEGVDBDHQWRRFAGNLAAG  120
OY      121  GAAGATSLCFVYPLDFARTRLAADVGR- AOREPFGLDCCIIRKPSDGLRGLYOGFNS  179
Db      121  GAAGATSLCFVYPLDFARTRLAADVGR- AOREPFGLDCCIIRKPSDGLRGLYOGFNS  180
OY      180  VOGIIYRAAFVGYIDTAKGMLPDPKKNHIVFSWMI AOSVTAVAGLLSYPPFTVRRRMM  239
Db      181  VOGIIYRAAFVGYIDTAKGMLPDPKKNHIVISWMI AOTVTAVALTLSPFTVRRRMM  240
OY      240  QSGRGADIMYTGTVDCMRKIAKDEGKAFFGAMSNNLRGGAFAVLVLDEIKKY  296
Db      241  QSGRGADIMYTGTVDCMRKIAKDEGKAFFGAMSNNLRGGAFAVLVLDEIKKY  297

RESULT 5
US-09-811-094-32
: Sequence 32, Application US/09811094
: Patent No. US2001004144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
: FILE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D4
: CURRENT APPLICATION NUMBER: US/09/811,094
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
US-09-811-094-32

Query Match      89.6%: Score 1391.5; DB 10; Length 298;
Best Local Similarity 88.6%: Pred. No. 3.4e-140;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1

OY      1  MGDHMSLAKFLAGAVAAAVSKTAVPIERYKLLIYOHASKOJSAEKYKGIIDCYVR  60
Db      1  MTDALSTAKDFLAGCAVAAAIKSTVAPIERKLLIYOHASKOJTADEKQYKGIIDCYVR  60
OY      61  IPKEGGLSFMGNLANIYIRFPQALNFAFDKXKOLFLEGVDBDHQWRRFAGNLAAG  120
Db      61  IPKEDEVLSFMGNLANIYIRFPQALNFAFDKXKOLFLEGVDBDHQWRRFAGNLAAG  120
OY      121  GAAGATSLCFVYPLDFARTRLAADVGR- AOREPFGLDCCIIRKPSDGLRGLYOGFNS  179
Db      121  GAAGATSLCFVYPLDFARTRLAADVGR- AOREPFGLDCCIIRKPSDGLRGLYOGFNS  180
OY      180  VOGIIYRAAFVGYIDTAKGMLPDPKKNHIVFSWMI AOSVTAVAGLLSYPPFTVRRRMM  239
Db      181  VOGIIYRAAFVGYIDTAKGMLPDPKKNHIVISWMI AOTVTAVALTLSPFTVRRRMM  240
OY      240  QSGRGADIMYTGTVDCMRKIAKDEGKAFFGAMSNNLRGGAFAVLVLDEIKKY  296
Db      241  QSGRGADIMYTGTVDCMRKIAKDEGKAFFGAMSNNLRGGAFAVLVLDEIKKY  297

RESULT 6
US-09-810-644-32
: Sequence 32, Application US/09810644

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: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveland, William
: APPLICANT: Willey, Sandra Eileen
: APPLICANT: Willet, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yazhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT).
: FILE REFERENCE: 660088.420D3
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 32
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien
: US-09-810-644-32
:
: Query Match      89.68; Score 1391.5; DB 10; Length 298;
: Best Local Similarity 88.68; Pred. No. 3,4e-140;
: Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
:
: Oy      1 MGDHMSFLKDFLAGVAAAVSKTAVAPLERVKLLQYOHASKQISAEKQYKGIIDCVNR 60
: Db      1 MTDALSFADFLAGVAAAIKSTAVAPLERVKLLQYOHASKQITADQYKGIIDCVNR 60
: Oy      61 IPKEQGLSFWRGNLANVIRYPTQALNFAFDKTKQFLTSGVDNRHKQFWRYPAGNLASG 120
: Db      61 IPKEQGLSFWRGNLANVIRYPTQALNFAFDKTKQFLTSGVDNRHKQFWRYPAGNLASG 120
: Oy      121 GAAGATSLCTVYLPDARTRLAADNGRR-AQREPHGLSDCIIFKSGDLGTYGFNVNS 179
: Db      121 GAAGATSLCTVYLPDARTRLAADNGRR-AQREPHGLSDCIIFKSGDLGTYGFNVNS 180
: Oy      180 VGGIITRAYFECVYPTAGKMLPDPKNVHIFPSMHIADSVYAVAGLLSYPDYRRRMM 239
: Db      181 VGGIITRAYFECVYPTAGKMLPDPKNVHIVISMHIADSVYAVAGLLSYPDYRRRMM 240
: Oy      240 QSGRKGADIMYGTGYDCMRRIAKDEGAKAFKFGANSNVLRCMGCAFVLYLDEIKKY 296
: Db      241 QSGRKGADIMYGTGYDCMRRIAKDEGAKAFKFGANSNVLRCMGCAFVLYLDEIKKY 297
:
: RESULT 7
: US-09-185-904A-33
: Sequence 33, Application US/09185904A
: Patent No. US20020177185A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveland, William
: APPLICANT: Willey, Sandra Eileen
: APPLICANT: Willet, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
: TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSA.
: TITLE OF INVENTION: THEREFOR
: FILE REFERENCE: 660088.420
: CURRENT APPLICATION NUMBER: US/09/185,904A
: CURRENT FILING DATE: 1998-11-03
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 33
: LENGTH: 298
: TYPE: PRT
: ORGANISM: Homo sapien

```

US-09-185-904A-33

Query Match	89.2%;	Score 1385.5;	DB 9;	Length 298;
Best Local Similarity	87.2%;	Pred. No. 1.5e-139;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

RESULT 8
US-09-811-094-33

```

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yezhong

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (AMT)
FILE REFERENCE: NOVEL AMT LIGANDS AND SCREENING ASSAYS THEREFOR
CURRENT APPLICATION NUMBER: 660088.42004
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
IS-09-811-094-33

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Query Match	89.2%	Score 1385.5;	DB 10;	Length 298;
Best Local Similarity	87.2%	Pred. No. 1.5e-139;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1;

[illegible]

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Qy      240 QSGRKADIMYTGTVDCWNRKIAKDEGAKAFPKGAMSVNLRGNGCAFVLVLYDELKKVV 297  
        |||  
Db      241 QSGRKGADIMYTGTVDCKWRKIIFREGGKAFFFKGAMSVNLRGNGCAFLVLVYLDELKKVI 298
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```

Applicant:	Anderson, Christen M.
Applicant:	Davis, Robert E.
Applicant:	Clevenger, William
Applicant:	Wiley, Sandra Eileen
Applicant:	Miller, Scott M.
Applicant:	Seabo, Tomas R.
Applicant:	Goshu, Soumitra S.
Applicant:	Moos, Walter H.
Applicant:	Pel, Yezhong
Title of Invention:	PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
Title of Invention:	NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
File Reference:	660088.420D3
Current Application Number:	US/09/810,644
Current Filing Date:	2001-03-14
Number of Seq. ID NOS:	37
Software:	FastSeq for Windows Version 3.0
Seq ID NO	33
Length:	298
Type:	PROT
Organism:	Homo sapien
US-09-810-644-33	

Query Match	89.2%:	Score 1385.5:	DB 10:	Length 298:
Best Local Similarity	87.2%:	Pred. No. 1,5e+139:		
Matches 260:	Conservative 21:	Mismatches 16:	Indels 1:	Gaps 1

OY	1	MGDAHSPLKDFLGAANAASKTAVAPAEIVKTLLOVNAHNOISAEKYOIKIIIDCVR	60
DB	1	MTGQALSPFKDDLAGIAAISKTRVAPAEIVKTLLOVNAHNOISAEKYOIKGIIVDCIVR	60
OY	61	IPKEGDFLSPWGNLANVIRYFPQALNFAFKDKYKOLFLGCVDRHKOFWRYPAGNIIASG	120
DB	61	IPKEGCVLSFPMGNLANVIRYFPQALNFAFKDKYKOLFLGCVDRKHTOFWRYPAGNIIASG	120
OY	121	GAGGATSLCFVYPLDFAFTRILAAVDYGR-AQREHFGLCDLIIKIFPSDGLRGLYCOFPNS	179
DB	121	GAGGATSLCFVYPLDFAFTRILAAVDGKSGTEREFRGLDCLVITKSDGIRGLYCOFPSVS	180
OY	180	VGGIILYRAAYRGVDTAKGMLPPEKNVHIFVSMWIKOSYTAVMKLLSYPFDFVRRRRMM	239
DB	181	VGGIILYRAAYRGVDTAKGMLPPEKNVHIVSMWIKOTYTAAGVASYPFDFVRRRRMM	240
OY	240	OSGRKGADIMTGYTDCRKLAKDEGAKAFKGMASVNLKMGCAFLVLYDEIKKTV	297
DB	241	OSGRKGADIMTGYTDCRKLAKDEGAKAFKGMASVNLKMGCAFLVLYDEIKKTV	298

Query Match	89.28;	Score 1385.5;	DB 10;	Length 298;
Best Local Similarity	87.28;	Pred. No. 1.5e-139;		
Matches 260;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1

[illegible]

RESULT 10
US-09-801-368-252
; Sequence 252, Application US/09801368

APPLICANT:	Busby, Robert
APPLICANT:	Call, Brian
APPLICANT:	Hiecht, Peter
APPLICANT:	Holtzman, Doug
APPLICANT:	Madden, Kevin
APPLICANT:	Maxon, Mary
APPLICANT:	Milne, Todd
APPLICANT:	No. US20020128250A1man, Theas
APPLICANT:	Royer, John
APPLICANT:	Salama, Sofie


```

RESULT 13
US-09-864-761-36440
Sequence 36440, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmica-x-1
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US/09/864,761
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: CB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 36440
LENGTH: 87
TYPE: PRt
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO L78810.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.2
OTHER INFORMATION: EXPRESSED IN HBLL00, SIGNAL = 10
OTHER INFORMATION: EXPRESSED IN FBTL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 7.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.7
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2
OTHER INFORMATION: SWISSPROT HIT: P05141, EVALU6 6.00e-38
OTHER INFORMATION: EST_HUMAN HIT: AW935235.1, EVALU6 5.00e-37
US-09-864-761-36440

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[illegible]

SEQ ID NO 2
LENGTH: 477
TYPE: PRT
ORGANISM: Homo sapiens
US-09-777-921A-2

Query Match 22.3% Score 346.5; DB 10; Length 477;
Best Local Similarity 32.7%; Pred. No. 1.9e-28;
Matches 96; Conservative 55; Mismatches 116; Indels 27; Gaps 10;

OY 10 KDLACAVAAVSKTAVAPIERVKLLQVHASKOISAEKQYKGIIDCVRIPEQGFLS 69
DB 196 RQLLAGGIAGAVSRTSTAPLDRLKIMQV-HGSK---SDKM-NIPGGFROMVKEGGIRS 249
OY 70 FWRGNLANVIRYPTOLNFAFKDKYKQLFLGVDRHKQFWRFFAGNLASGAAGATSLC 129
DB 250 LMRGNGTNVJIKIAPETAVKFMAVEQYKKLLTEEGCKICTFERFISGSM---AGATAOT 304
OY 130 FVYPLDFARPLADVGRRAQREPHGLGDCI IKIFKSDGLKGLYOGFNVSVQGIITYRAA 189
DB 305 FIYPMKWKTRLA--VGKTGO--YSGIYDCAKKILKHGGLGAFYKGYVNNLGIIPYAGI 360
OY 190 YFGVYDTAK-----GMLPDPKKNVHIFVSMIAQSVTAAGLLSTYPPDTRRRMMMSGRK 244
DB 361 DLAVYELLSKSYWLDNPAKDSVNPQVWLLGGCALSTCCQLASTPLALVTRRMOQAMLE 420
OY 245 GADIWYTGVDCKRKIAKDEGAKAFKGAWSN---VLKMGGAFLVLYDEIKK 295
DB 421 GSPQL--NMVGLFRRIISKEGICPLYRGITFPNFMKVLPAVCISY--VVEENMKO 470

Search completed: June 18, 2003, 13:32:46
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2003, 13:32:22 ; Search time 40 Seconds

(without alignments)
713.798 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDLFAGAVAAA.....LRGMCAGFVLVLYDEIKKYV 297

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1526.5	98.3	298	1	A44778	ADP,ATP carrier pr
2	1466.5	94.4	298	2	I60173	adenine nucleotide
3	1463.5	94.2	298	2	S37210	ADP,ATP carrier pr
4	1458.5	93.9	298	1	XWBO	ADP,ATP carrier pr
5	1391.5	89.6	298	1	A29132	ADP,ATP carrier pr
6	1385.5	89.2	298	1	S03894	ADP,ATP carrier pr
7	1380.5	88.9	298	2	B43646	ADP,ATP carrier pr
8	1368.5	88.1	298	2	S31814	ADP,ATP carrier pr
9	1142.5	73.6	301	1	S31935	ADP,ATP carrier pr
10	1045.5	67.3	313	2	T25850	hypothetical prote
11	1043.5	67.2	313	2	T23207	hypothetical prote
12	1037.5	66.8	300	2	T25371	hypothetical prote
13	1005.5	64.7	300	2	T15206	hypothetical prote
14	973.5	62.7	339	2	A41677	ADP,ATP carrier pr
15	904.5	58.2	301	2	S51132	ADP,ATP carrier pr
16	772	49.7	306	2	T20012	hypothetical prote
17	770.5	49.6	308	1	S30259	ADP,ATP carrier pr
18	756.5	48.7	387	2	S14876	ADP,ATP carrier pr
19	752.5	48.5	322	2	T40526	ADP,ATP translocas
20	752.5	48.5	386	2	T09709	ADP,ATP carrier pr
21	751.5	48.4	387	2	S16568	ADP,ATP carrier pr
22	746.5	48.1	379	2	T04608	ADP,ATP carrier pr
23	746.5	48.1	382	2	S33630	ADP,ATP carrier pr
24	745.5	48.0	326	2	T25728	hypothetical prote
25	745.5	48.0	386	2	S17917	ADP,ATP carrier pr
26	744.5	47.9	386	2	S21974	ADP,ATP carrier pr
27	740	47.6	379	2	S21313	ADP,ATP carrier pr
28	740	47.6	386	2	S14874	ADP,ATP carrier pr
29	737	47.5	385	1	S29852	ADP,ATP carrier pr

ALIGNMENTS

```

RESULT 1
A44778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C>Date: 17-Mar-2000 #sequence,revision 17-Mar-2000 #text,change 17-Mar-2000
C:Accession: A44778; S03893; A59891; A28116
R:Li, K.; Warner, C.K.; Hodge, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Mae
J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, 1s
A:Reference number: A44778; MUID:89340495; PMID:2547778
A:Accession: A44778
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <L1A>
A:Cross-references: GB:J04982; NID:g178658; PIDN:AAA51736.1; PID:g178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial AC
A:Reference number: S03893; MUID:89236396; PMID:2541251
A:Accession: S03893
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <CO2>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of
A:Reference number: A39891; MUID:86041145; PMID:2823266
A:Accession: A39891
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', '17-146, 'RR', '149, '151-226, 'L', '228-298 <NEC>
A:Cross-references: GB:J02966; NID:g339919; PIDN:AAA61223.1; PID:g339920
R:Houlsworth, J.; Altardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA 1e
A:Reference number: A94197; MUID:88124845; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:g339724; PIDN:AAA67571.1; PID:g339725
A:Experimental source: liver
C:Genetics:
A:Gene: GDB:ANT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
A:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

```

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1: Length 298;
Best Local Similarity 98.3%; Pred. No. 1.6e-130;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 180
OY 180 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 239
DB 181 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 240
OY 240 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 298

RESULT 2

160173

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 160173

R:Shiohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427

C:Genetics:

A:Gene: ant1

A:Introns: 37/3: 200/1: 247/1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2: Length 298;
Best Local Similarity 94.3%; Pred. No. 4.3e-125;
Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 180
OY 180 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 239
DB 181 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 240
OY 240 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 298

DB 241 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 298

RESULT 3

S37210

ADP,ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R: Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <LAP>

A:Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628

C:Genetics:

A:Gene: ANCI

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2: Length 298;
Best Local Similarity 94.0%; Pred. No. 8e-125;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

OY 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
DB 1 MCDHMSFLKDFLAGVAAVSKTAVAPLERVKLLLOVHASKOISAEKQYGIIDCVRR 60
OY 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
DB 61 IREKQGLSFWMGNLANVIRYPTQALNFAPKDKYKQFLGCVDRHKQFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAOREFHGLGDCIIRKFSKDLKGLYOGFNV 180
OY 180 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 239
DB 181 VOGIITIRAAVFGVYDTAKGMLPDPKNNHIFVSMIAOSVTAVAGLVSPFDTVRRRMM 240
OY 240 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 297
DB 241 QSGRKADIMYTGTVDCMKRIKADGAKAFPGKAGMSNVLRGGAFLVLYDEIKKYV 298

RESULT 4

XMB0

ADP,ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C>Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

R: Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differ

A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <POM>

A:Cross-references: GB:M24102; NID:g529414; PIDN:AAA30768.1; PID:g529415

R: Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an

A:Reference number: A24822; MUID:86295775; PMID:3017341

A:Accession: A24822

A:Molecule type: mRNA

A:Residues: 208-298 <RAS>

A:Gene: GDB:ANT3: ANT3Y
A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3
A:Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and GDB:
C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:1-298/Product: ADP,ATP carrier protein status predicted <MA>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 89.2%; Score 1385.5; DB 1: Length 298;
Best Local Similarity 87.2%; Pred. No. 9.1e-118;

Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

OY 1 MCDHANSFLKDFLAGVAAVASTAVAPIERVKLLLOVHASKOISAEKQYKIIDCVVR 60
1 MPEQATISPAKDFLAGGIAAIAISTAVAPIERVKLLLOVHASKOIAADQYKIVDCIYR 60
DB 1 MPEQATISPAKDFLAGGIAAIAISTAVAPIERVKLLLOVHASKOIAADQYKIVDCIYR 60
OY 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
1 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
DB 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 180
OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 240
OY 240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
DB 241 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298

RESULT 7

B43646

ADP,ATP carrier protein T2 - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
C:Accession: B43646
R.Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
Biochemistry 28, 866-873, 1989
A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
A:Reference number: A43646; MUID:89229093; PMID:2540808
A:Accession: B43646
A:Status: preliminary
A:molecule type: mRNA
A:Residues: 1-298 <POM>
A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.9%; Score 1380.5; DB 2: Length 298;
Best Local Similarity 86.9%; Pred. No. 2.6e-117;

Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

OY 1 MCDHANSFLKDFLAGVAAVASTAVAPIERVKLLLOVHASKOISAEKQYKIIDCVVR 60
1 MPEQATISPAKDFLAGGIAAIAISTAVAPIERVKLLLOVHASKOIAADQYKIVDCIYR 60
DB 1 MPEQATISPAKDFLAGGIAAIAISTAVAPIERVKLLLOVHASKOIAADQYKIVDCIYR 60
OY 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
1 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
DB 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 180

OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 240
OY 240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297
DB 241 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 298

RESULT 8

S31814

ADP,ATP carrier protein T2 - mouse
N:Alternate names: adenine nucleotide translocase
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
C:Accession: S31814
R.Costet, P.; Laplace, C.
submitted to the EMBL Data Library, January 1993
A:Reference number: S31814
A:Accession: S31814
A:Status: preliminary
A:molecule type: mRNA
A:Residues: 1-298 <COS>

A:Cross-references: EMBL:X70847
C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 88.1%; Score 1368.5; DB 2: Length 298;
Best Local Similarity 87.2%; Pred. No. 3.2e-116;

Matches 259; Conservative 18; Mismatches 19; Indels 1; Gaps 1;

OY 1 MCDHANSFLKDFLAGVAAVASTAVAPIERVKLLLOVHASKOISAEKQYKIIDCVVR 60
1 MCDHANSFLKDFLAGVAAVASTAVAPIERVKLLLOVHASKOISAEKQYKIIDCVVR 60
DB 1 MCDHANSFLKDFLAGVAAVASTAVAPIERVKLLLOVHASKOISAEKQYKIIDCVVR 60
OY 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
1 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
DB 61 IPEQGFSLFWMKGNLANVIRYPTQALNFAFKDKYKQLFGVDHKKOFWRFFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIIKIFKSDGLRGLYOGFNV 180
OY 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
180 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 239
DB 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTIIFVSMIAQSVTLVAGVSTPFDVRRRM 240
OY 240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 296
240 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 296
DB 241 QSGRKADIMYGTVDCKWKIRAKDEGAKAFKGCAMSNVLRGCGAFVLVYDEIKKY 297

RESULT 9

S31935

ADP,ATP carrier protein - African malaria mosquito
C:Species: Anopheles gambiae (African malaria mosquito)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S31935; S31936
R.Beard, C.B.; Crews-Oyen, A.E.; Collins, F.H.
submitted to the EMBL Data Library, February 1993
A:Description: A cDNA encoding an ADP/ATP carrier from the mosquito Anopheles gambiae
A:Reference number: S31935
A:Accession: S31935
A:Status: preliminary
A:molecule type: DNA
A:Residues: 1-301 <BEA>

A:Cross-references: EMBL:221814; EMBL:221815
C:Superfamily: ADP,ATP carrier protein: ADP,ATP carrier protein repeat homology
C:Keywords: duplication; transmembrane protein
F:7-101/Domain: ADP,ATP carrier protein repeat homology <ACP1>

OY 8 FLKDFLAGAANAASKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 67
 12 FLIDLASGCTAAASVSTAAVPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 71
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAGATS 127
 72 AALMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAGATS 131
 OY 128 LCFVYPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII1YR 187
 132 LCFVYPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII1YR 191
 OY 188 AAFVGYVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGRKGA 246
 192 AAFVGYVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGRKGA 249
 OY 247 DIMYGTGVDGMRKRIADKCAKAFKFGAMSNNVLRGMGCAVLYLYDEIKRYV 297
 250 DILYKNTLDCAKK11ONEGMSAMFKGALSNNVFRGTCGALVLYLYDEIKRYV 300

RESULT 13

T13206

hypothetical protein W02D3.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C:Accession: T13206

R:Le, T.; Weinstock, L.; Rifkin, L.

Submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans cosmid W02D3.

A:Reference number: 218308

A:Accession: T13206

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <LET>

A:Cross-references: EMBL:AF003141; NID:92088732; PID:92088738; PIDN:AA854179.1; GSPDB:GN

A:Experimental source: strain Bristol N2; clone W02D3

C:Genetics:

A:Gene: CESP:W02D3.6

A:Map position: 1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F:9-103/Domain: ADP,ATP carrier protein repeat homology <ACR>

Query Match

Best Local Similarity 64.7%; Score 1005.5; DB 2; Length 300;

Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;

OY 8 FLKDFLAGAANAASKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 67
 12 FLIDLASGCTAAASVSTAAVPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKEGF 71
 OY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAGATS 127
 72 AALMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAGATS 131
 OY 128 LCFVYPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII1YR 187
 132 LCFVYPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII1YR 191
 OY 188 AAFVGYVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGRKGA 246
 192 AAFVGYVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGRKGA 249
 OY 247 DIMYGTGVDGMRKRIADKCAKAFKFGAMSNNVLRGMGCAVLYLYDEIKRYV 297
 250 DILYKNTLDCAKK11ONEGMSAMFKGALSNNVFRGTCGALVLYLYDEIKRYV 300

RESULT 14

A41677

ADP,ATP carrier protein - Chlorella kessleri

C:Species: Chlorella kessleri

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: A41677
 R:Higharth, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A:Title: Glucose increases the expression of the ATP/ADP translocator and the 91
 A:Reference number: A41677; MUID:92084708; PMID:1748677
 A:Accession: A41677
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HIL>
 A:Cross-references: GB:M76669; NID:9516596; PIDN:AAA33027.1; PID:9516597
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; mitochondrial; transmembrane protein
 F:38-134/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:144-235/Domain: ADP,ATP carrier protein repeat homology <ACPI>
 F:241-329/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match

Best Local Similarity 62.7%; Score 973.5; DB 2; Length 339;

Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

OY 7 SFLKDFLAGAANAASKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 64
 40 AFDKDLGAGTGAISKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 99
 OY 65 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAG 124
 100 OGVSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAG 158
 OY 125 ATSLCFVYPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII 184
 159 ACSLLIYVPLDFARTRRLADVGRRAORFHLGDCI1K1FKSDGLRGLYOGFNVSVGII 218
 OY 185 IYRAAYFGVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGR 243
 219 YVRGAYFGVYDTRAKGML-PDPKRVNHI FVSMWIAQSVTAVAGLLSYPFQVVRRRMMQSGR 276
 OY 244 KCADIMYGTGVDGMRKRIADKCAKAFKFGAMSNNVLRGMGCAVLYLYDEIKRYV 297
 277 -GGEROYNGTIDCMRVAOQECMAKAFKFGAMSNNVLRGMGCAVLYLYDEIKRYV 329

RESULT 15

S51132

ADP,ATP carrier protein - malaria parasite (Plasmodium falciparum)

N:Alternate names: ADP/ATP transporter

C:Species: Plasmodium falciparum

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C:Accession: S58993; S51132

R:Hatlin, J.; Jauregui, J. G.

Eur. J. Biochem. 228, 86-91, 1995

A:Title: Molecular characterisation of the ADP/ATP-translocator cDNA from the hum

A:Reference number: S58993; MUID:95188918; PMID:7883016

A:Accession: S58993

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-301 <HAT>

A:Cross-references: EMBL:X83551; NID:9623334; PIDN:CA58541.1; PID:9623335

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:6-102/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:112-203/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:209-301/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match

Best Local Similarity 58.2%; Score 904.5; DB 2; Length 301;

Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

OY 7 SFLKDFLAGAANAASKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 64
 40 AFDKDLGAGTGAISKTAVAPIERVKLLLOVOHASKOISAEKYOYKGIIDCVVRIPKE 99
 OY 65 OGFLSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAG 124
 100 OGVSFMRGNLANVIRYPTQALNFAFKDKYKQFLGCVDRHKKOFMRYPFAGNLASGAG 158

Db 68 GGVLSLMRGNNVNIIRVPTQAFNFRAPKDYFNINIF-PRRDQNTDPSKFFCVNLLSQTATG 126

QY 125 ATSLCEVVYPLDFAFTRRLAADVNGRAOREBHEGLGDCITIKIFKSDGLRGILYOGFNVSVOGII 184

Db 127 AISLLIYPLDFAFTRRLASIDCKGKDROFTGLFDCIAKIKYKOTGLSLTSFGCVSVTGII 186

QY 185 IYRAAYPCVYDTAKAML-PDDRKNVHIFVSHMLAOSVTAAGLLSYFDIVRRRMHMOGSE 243

Db 187 VYRGSGYFCLYDSAKALLFTNDKNTNIIYLMKMAAOSVTIAGLISYFPFDIVRRRMHMSG 246

QY 244 KG-ADIMYTGVDRCRIAKIDEGAKAFKFGAVSNVLRGMSGFVILVYOEIKKYV 297

Db 247 KGEETIYKNTIIDCMITILRNEGKFGFFGGAANAIRKGGAGALVILFYVELQQLI 301

Search completed: June 18, 2003, 13:36:47
Job time : 41 secs

GenCore version 5.1.6
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CM protein - protein search, using sw model

Run on: June 18, 2003, 13:28:56 ; Search time 22 Seconds

(without alignments)
559,930 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAAA.....LRMGCAFVLVLDEIKYV 297

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1526.5	98.3	298	1 ADT1_HUMAN	P12235 homo sapien
2	1466.5	94.4	298	1 ADT1_RAT	O05962 rattus norv
3	1463.5	94.2	298	1 ADT1_MOUSE	P48962 mus musculu
4	1453.5	93.6	297	1 ADT1_BOVIN	P02722 bos taurus
5	1408.5	90.7	298	1 ADT2_MOUSE	P51881 mus musculu
6	1407.5	90.6	298	1 ADT2_RAT	O09073 rattus norv
7	1398.5	90.1	298	1 ADT2_HUMAN	P05141 homo sapien
8	1385.5	89.2	298	1 ADT3_HUMAN	P12236 homo sapien
9	1380.5	88.9	298	1 ADT3_BOVIN	P32007 bos taurus
10	1211	78.0	297	1 ADT_DROME	O26365 drosophila
11	1162.5	74.9	301	1 ADT_ANOGA	O27238 anopheles g
12	973.5	62.7	339	1 ADT_CHLKE	P31692 chlorella k
13	770.5	49.6	308	1 ADT_CHLRE	P27080 chlamydomon
14	756.5	48.7	387	1 ADT1_MAIZE	P04709 zea mays (m
15	753.5	48.5	322	1 ADT_SCHPO	O09188 schizosach
16	752.5	48.5	386	1 ADT1_GOSHI	O22342 gossypium h
17	751.5	48.4	382	1 ADT_ORYSA	P31691 oryza sativ
18	751.5	48.4	387	1 ADT2_MAIZE	P12857 zea mays (m
19	746	48.0	381	1 ADT1_ARATH	P31167 arabidopsis
20	744.5	47.9	386	1 ADT1_SOLTU	P25083 solanum tub
21	742.5	47.8	331	1 ADT1_MHEAT	O41629 triticum ae
22	740	47.6	386	1 ADT2_SOLTU	P27081 solanum tub
23	736	47.4	307	1 ADT3_YEAST	P18238 saccharomyc
24	734	47.3	318	1 ADT2_YEAST	P18239 saccharomyc
25	733.5	47.2	313	1 ADT_NEUCR	P07723 neurospora
26	731	47.1	385	1 ADT2_KLUFA	P40941 kluyveromyc
27	729	46.9	305	1 ADT1_KLUFA	O49382 kluyveromyc
28	728.5	46.9	331	1 ADT2_MHEAT	O41630 triticum ae
29	718.5	46.3	309	1 ADT1_YEAST	P04710 saccharomyc
30	302.5	19.5	678	1 CMCI_HUMAN	O75746 homo sapien
31	300.5	19.3	330	1 GDC_BOVIN	O01888 bos taurus
32	296.5	19.1	702	1 CMCI_CAEBL	O21153 caenorhabdi
33	296	19.1	588	1 CMCI_CAEBL	O20799 caenorhabdi

34	295	19.0	322	1 GDC_RAT	P16261 rattus norv
35	292.5	18.8	307	1 ODC2_YEAST	O99297 saccharomyc
36	292	18.8	332	1 GDC_HUMAN	P16260 homo sapien
37	291	18.7	675	1 CMCI_HUMAN	O90350 homo sapien
38	286	18.4	587	1 CMCI_CAEBL	O19529 caenorhabdi
39	280	18.0	315	1 MPT_HUMAN	O9h2d1 homo sapien
40	279.5	18.0	676	1 CMCI_MOUSE	O9qxx4 mus musculu
41	270.5	17.4	315	1 SAI8_HUMAN	O9h1k4 homo sapien
42	267.5	17.2	325	1 UCP5_MOUSE	O9z2b2 mus musculu
43	266.5	17.2	310	1 ODC1_YEAST	O03028 saccharomyc
44	265.5	17.1	325	1 UCP5_HUMAN	O95258 homo sapien
45	263.5	17.0	695	1 CMCI_DROME	O9va73 drosophila

ALIGNMENTS

RESULT 1	ID	ADT1_HUMAN	STANDARD:	PRT:	298 AA.
AC	P12235:				
DT	01-OCT-1989 (Rel. 12, Created)				
DT	01-NOV-1990 (Rel. 16, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	ADP,ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1).				
GN	SLC25A4 OR ANT1.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=89236396; PubMed=2541251;				
RA	Cozens A.L., Runswick M.J., Walker J.E.;				
RT	"DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase.";				
RT	J. Mol. Biol. 206:261-280(1989).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=89340499; PubMed=2547778;				
RA	Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,				
RA	Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;				
RT	"A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed.";				
RT	J. Biol. Chem. 264:13998-14004(1989).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RP	MEDLINE=86041149; PubMed=2823266;				
RA	Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;				
RT	"cDNA sequence of a human skeletal muscle ADP/ATP translocator: Jack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE-EYE:				
RC	Strausberg R.;				
RA	Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.				
RN	[5]				
RP	SEQUENCE OF 1-37 FROM N.A.				
RP	TISSUE-LIVER:				
RC	MEDLINE=88124845; PubMed=2829183;				
RA	Houldsworth J., Altardi G.;				
RT	"Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in adult human liver.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).				
RN	[6]				
RP	VARIANTS PEO PRO-114 AND MET-289.				
RP	MEDLINE=20385067; PubMed=10926541;				
RA	Kaukonen J., Jusselien J.K., Tiranti V., Kyttala A., Zeviani M.,				
RA	Conti G.P., Kertanen J., Pellonen L., Suomalainen A.;				
RT	"Role of adenine nucleotide translocator 1 in mtDNA maintenance.";				

RL Science 289:782-785(2000).
CC -i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -i- SUBUNIT: HOMODIMER.
CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -i- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
CC progressive external ophthalmoplegia with various mitochondrial
CC DNA deletions (PEO). Patients with PEO have mitochondrial
CC myopathy, progressive external ophthalmoplegia, and other
CC abnormalities associated with multiple different deletions of
CC mitochondrial DNA.
CC
CC -i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
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CC
CC EMBL: J02966; AAA61223.1; -
CC EMBL: J03593; AAA36751.1; -
CC EMBL: J04982; AAA51736.1; -
CC EMBL: BC008664; AAH08664.1; -
CC PIR: A28116; A28116.
CC PIR: A39891; A39891.
CC PIR: S03893; S03893.
CC PIR: A44778; A44778.
CC Genew: HGNC:10990; SLC25A4.
CC MIM: 103220; -
CC MIM: 157640; -
CC
CC InterPro: IPR002067; Mtl_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC
CC Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport;
CC
CC Multigene family: Disease mutation.
CC
CC TRANSMEM 12 29 1 (POTENTIAL).
CC TRANSMEM 73 91 2 (POTENTIAL).
CC TRANSMEM 117 134 3 (POTENTIAL).
CC TRANSMEM 176 195 4 (POTENTIAL).
CC TRANSMEM 214 231 5 (POTENTIAL).
CC TRANSMEM 273 291 6 (POTENTIAL).
CC REPEAT 1 110 1.
CC REPEAT 111 208 2.
CC REPEAT 209 298 3.
CC
CC VARIANT 114 114 A -> P (IN PEO).
CC
CC VARIANT 289 289 V -> M (IN PEO).
CC
CC CONFLICT 16 16 /FTID-VAR_012111.
CC CONFLICT 147 149 G -> A (IN REF. 3).
CC CONFLICT 227 227 KGA -> RR (IN REF. 3).
CC
CC SEQUENCE 298 AA: 33064 MW: 59704FAEC4ETGFBF CRC64:
SQ
Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 2,3e-132;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

DB 121 GAAGATSLCFYVPLDFARTRLADYVGKGAQREFGLGDCIILKFSKDLGLYOGFNVS 180
OY 180 VGGIITRYANFGVDTAKKGLPDKKNHIFVSMIAOSVAVAGLSTPDTYARRMM 239
DB 181 VGGIITRYANFGVDTAKKGLPDKKNHIFVSMIAOSVAVAGLSTPDTYARRMM 240
OY 240 OSGRKADIMTGTDCARKIAKDEGAKAFKGSANVLRGCGAFVLYLDELKKYV 297
DB 241 OSGRKADIMTGTDCARKIAKDEGAKAFKGSANVLRGCGAFVLYLDELKKYV 298
RESULT 2
ADPT_RAT
ID ADPT_RAT STANDARD: PRT: 298 AA.
AC 005962:
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (adenine nucleotide translocator 1) (ANT1).
GN SLC25A4 OR ANT1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Sprague-Dawley, and Wistar; TISSUE=Heart, and Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinohara Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Biochim. Biophys. Acta 1152:192-196(1993).
CC -i- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -i- SUBUNIT: HOMODIMER.
CC -i- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -i- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
CC EXTENT, IN BRAIN AND KIDNEY.
CC -i- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -i- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC
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CC
CC EMBL: X61667; CAA43842.1; -
CC EMBL: D12770; BAA02237.1; -
CC InterPro: IPR002067; Mtl_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PF00153; mito_carr; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PROSITE: PS00215; MITOCH_CARRIER; 3.
CC
CC Mitochondrion: Inner membrane; Repeat: Transmembrane; Transport;
CC
CC Multigene family.
CC
CC TRANSMEM 12 29 1 (POTENTIAL).
CC TRANSMEM 73 91 2 (POTENTIAL).
CC TRANSMEM 117 134 3 (POTENTIAL).
CC TRANSMEM 176 195 4 (POTENTIAL).
CC TRANSMEM 214 231 5 (POTENTIAL).
CC TRANSMEM 273 291 6 (POTENTIAL).
CC REPEAT 1 110 1.
CC REPEAT 111 208 2.
CC REPEAT 209 298 3.
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CC SEQUENCE 298 AA: 33298 MW: 66704FF78C6BC320 CRC64:
SQ
Query Match 94.4%; Score 1466.5; DB 1; Length 298;
Best Local Similarity 94.3%; Pred. No. 7e-127;


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RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
RN [2]
RP SEQUENCE.
RX MEDLINE-82188267; Pubmed-7076130;
RA Aquila H., Misra D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria."
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP SEQUENCE OF 207-297 FROM N.A.
RX MEDLINE-86295775; Pubmed-3017341;
RA Rasmussen U.B., Wohlrab H.;
RT "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3' noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A03181; XMOO.
DR PIR: A24822; A24822.
DR PIR: A43646; A43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mito_carr_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER_3.
KN Mitochondrion: Inner membrane: Repeat: Transmembrane: Transport;
KN Multigene family: Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A4A0EB48 CRC64;

Query Match 93.6%; Score 1453.5; DB 1; Length 297;
Best Local Similarity 94.6%; Pred. No. 1; 1e-125;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 3 DHAMSLKDLFAGAAVAASKTAVADIERVKLLQVQHASKQISAQKYGKIIDCVVRIP 62
DB 2 DQALSLKDLFAGVAAIAISKTAVADIERVKLLQVQHASKQISAQKYGKIIDCVVRIP 61
OY 63 KEGGLSPFMRGNLANIYRFPFOALNFAFKDKYKOLFICGVDRHKKFWRFPAGNLSGGA 122
DB 62 KEGGLSPFMRGNLANIYRFPFOALNFAFKDKYKOLFICGVDRHKKFWRFPAGNLSGGA 121
OY 123 AGATSLCFVYPLDFARTRLAADGR-RAOREFHGLDGCIIKPKSGGLGLOCFVNSVO 181
|||||

DB 122 AGATSLCFVYPLDFARTRLAADGR-RAOREFHGLDGCIIKPKSGGLGLOCFVNSVO 181
OY 182 GIITRYRAAFGVYDTAKGMLPDPKNVHI FVSMWIAQSVTAAGLLSYFPDTRRRMMQS 241
DB 182 GIITRYRAAFGVYDTAKGMLPDPKNVHI IYSWMIAQSVTAAGLLSYFPDTRRRMMQS 241
OY 242 GRGADIMYTGTYDCMKRIKADGAKAFKFGANSNVLKRGCAFVLVYDEIKKYV 297
DB 242 GRGADIMYTGTYDCMKRIKADGPKAFKFGANSNVLKRGCAFVLVYDEIKKYV 297

RESULT 5
ADP2_MOUSE STANDARD: PRT: 298 AA.
ID ADP2_MOUSE
AC P51881; 061311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE-97059403; Pubmed-8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs."
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Costet P., Laplace C.;
RL Submitted (Feb-1993) to the EMBL/Genbank/DBJ databases.
RN [4]
RP REVISIONS.
RA Laplace C.;
RL Submitted (Feb-1997) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-20432087; Pubmed-10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL: U27316; AAC52838.1; -
DR EMBL: U10404; AAA19009.1; -
DR EMBL: X70847; CAA50196.1; -

```


RX MEDLINE-90375457; PubMed-2168878;
 RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurel J.;
 RT "The human fibroblast adenine nucleotide translocator gene. Molecular
 cloning and sequence.";
 RL J. Biol. Chem. 265:16060-16063(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-87166056; PubMed-3031073;
 RA Bactini R., Ferrati S., Kaczmarek L., Calabretta B., Chen S.T.,
 RA Baserga R.;
 RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
 RT growth-regulated.";
 RL J. Biol. Chem. 262:4355-4358(1987).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Chen C.N., Su Y., Baydayan P., Strano A., Nagaraia R.,
 RA Mazzarella R.A., Schlessinger D., Chen E.Y.;
 RL Submitted (JUN-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Becker M., Graves T., Ozerky P.;
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 47-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-86124845; PubMed-2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC
 DR EMBL: M57424; AAA51737.1; -;
 DR EMBL: J02683; AAA35579.1; -;
 DR EMBL: L78810; AAB39266.1; -;
 DR EMBL: AC004000; AAB96347.1; -;
 DR EMBL: J03591; AAA36749.1; -;
 DR PIR: A29132; A29132.
 DR PIR: C28116; C28116.
 DR Genew: HGNC:10991; SLC25A5.
 DR MIM: 300150; -;
 DR Interpro: IPR002067; Mit_carrier.
 DR Interpro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 6 6 V -> L (IN REF. 2).
 FT CONFLICT 66 66 G -> E (IN REF. 2).

FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
 FT CONFLICT 162 162 V -> G (IN REF. 5).
 SQ SEQUENCE 298 AA; 32895 MW; F973CAED92C49D3 CRC64;
 Query Match 90.1%; Score 1398.5; DB 1; Length 298;
 Best Local Similarity 88.9%; Pred. No. 1.2e-120;
 Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;
 OY 1 MCDHMSFLKDFLAGAANAASVAVAPLERYKLLIQVHASKQISAEKQYKGIIDCVRR 60
 1
 DB 1 MDAVAVFAKDFLAGAANAISKTVAAPLERYKLLIQVHASKQITADKQYKGIIDCVRR 60
 OY 61 IPEKGFSLFMRGNLANVIRYPTQALNFAFDKTKQLFLGCVDRHKQFWRPAGNLASG 120
 1
 DB 61 IPEKGFSLFMRGNLANVIRYPTQALNFAFDKTKQLFLGCVDRHKQFWRPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDPARTRLADYGRAR-AQREPIGLDCCIIKIKSDGLRGLYQGFNV 179
 1
 DB 121 GAAGATSLCFVYPLDPARTRLADYGRAR-AQREPIGLDCCIIKIKSDGLRGLYQGFNV 180
 OY 180 VGGIIVRAAYFGVYDTAKGMLPDKRNHIFVSNMIAQSVTAVAGLSTPFDVRRMM 239
 1
 DB 181 VGGIIVRAAYFGVYDTAKGMLPDKRNHIFVSNMIAQSVTAVAGLSTPFDVRRMM 240
 OY 240 OSGRGADIMTGTVDCKRKIAKDGAKAFKFGANSVLRGCGAFVLVDEIKKY 296
 1
 DB 241 OSGRGADIMTGTVDCKRKIAKDGAKAFKFGANSVLRGCGAFVLVDEIKKY 297
 RESULT 8
 ADT3_HUMAN
 ID ADT3_HUMAN STANDARD; PRT; 298 AA.
 AC P12236; O96C49;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP/ATP carrier protein, liver isoform 12 (ADP/ATP translocase 3)
 DE (adenine nucleotide translocator 3) (ANT 3).
 GN SLC25A6 OR ANT3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OC NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89236396; PubMed-2541251;
 RA Cozens A.L., Runswick M.J., Walker J.E.;
 RT "DNA sequences of two expressed nuclear genes for human mitochondrial
 RT ADP/ATP translocase.";
 RL J. Mol. Biol. 206:261-280(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
 RA Margolin J.F.;
 RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, Cervix, Eye, and Lung;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 36-298 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE-86124845; PubMed-2829183;
 RA Houldsworth J., Altardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.

```

-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
-----
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CC CC entities requires a license@lsb.ch). (See http://www.lsb.ch/announce/
CC CC or send an email to license@lsb.ch).
-----
DR EMBL: J03592; AAA36750.1; -
DR EMBL: AY007215; AAC01968.1; -
DR EMBL: BC007285; AAH07285.1; -
DR EMBL: BC007850; AAH07850.1; -
DR EMBL: BC008737; AAH08737.1; -
DR EMBL: BC008935; AAH08935.1; -
DR EMBL: BC014775; AAH14775.1; -
DR PIR: S03894; S03894.
DR PIR: B28116; B28116.
DR Genew: HGNC:10992; SLC25A6.
DR MIM: 300151; -
DR MIM: 403000; -
DR InterPro: IPR002067; Mtl_carrier.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mto_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSHEM 12 29 1 (POTENTIAL).
FT TRANSHEM 73 91 2 (POTENTIAL).
FT TRANSHEM 117 134 3 (POTENTIAL).
FT TRANSHEM 176 195 4 (POTENTIAL).
FT TRANSHEM 214 231 5 (POTENTIAL).
FT TRANSHEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT REPEAT 300 398 4.
FT CONFLICT 105 108 KHTO -> RHA (IN REF. 4).
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
SQ SEQUENCE 298 AA: 32866 MW: 18534EPF0E49672P CRC64.

Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. 1.8e-119;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHANSLKPLFLAGNAVAANSVKRAVAPIERVKLLLOVQAHNSKQISAKQYKGIIDCYR 60
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 1 MTEQALISPAKQFLAGIAAALISKTAVANPIERVKLLLOVQAHNSKQIAADAKQYKGIIDCYR 60

QY 61 IPKRGFLSPFRGNLANIYIRYEPQALNFAFKDKYKQFLGSDVDRHHKQFMYRFGAGNLASG 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 61 IPKRGQVLSFPRGNLANIYIRFPQALNFAFKDKYKQFLGSDVDRHHKQFMYRFGAGNLASG 120

QY 61 IPKRGQVLSFPRGNLANIYIRFPQALNFAFKDKYKQFLGSDVDRHHKQFMYRFGAGNLASG 120
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 61 IPKRGQVLSFPRGNLANIYIRFPQALNFAFKDKYKQFLGSDVDRHHKQFMYRFGAGNLASG 120

QY 121 GAACATSLCFPYPLDPFARTRLAADVGR-AQREFHGLGSDCIIRKIFKSDGLRGGLYOGFNVS 179
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 121 GAACATSLCFPYPLDPFARTRLAADVGR-AQREFHGLGSDCIIRKIFKSDGLRGGLYOGFNVS 179

QY 121 GAACATSLCFPYPLDPFARTRLAADVGR-AQREFHGLGSDCIIRKIFKSDGLRGGLYOGFNVS 179
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 121 GAACATSLCFPYPLDPFARTRLAADVGR-AQREFHGLGSDCIIRKIFKSDGLRGGLYOGFNVS 179

QY 180 VQGIILYRAAFVGYVDRPAKGLPPKKNVHIFVSMNLIQSVYAVAGLSYPRDYARRRRMM 239
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 180 VQGIILYRAAFVGYVDRPAKGLPPKKNVHIFVSMNLIQSVYAVAGLSYPRDYARRRRMM 239

QY 181 VQGIILYRAAFVGYVDRPAKGLPPKKNVHIFVSMNLIQSVYAVAGLSYPRDYARRRRMM 240
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 181 VQGIILYRAAFVGYVDRPAKGLPPKKNVHIFVSMNLIQSVYAVAGLSYPRDYARRRRMM 240

QY 240 QSGKRGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLKRMGGAFLVLYDELKRYV 297
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 241 QSGKRGADIMYTGTVDCWRKIAKDEGAKAFKGAWSNVLKRMGGAFLVLYDELKRYV 298

RESULT 9
ADPT3_BOVIN
ID ADPT3_BOVIN STANDARD: PRT: 298 AA.
NC P32007;
DT 01-JUL-1993 (Rel. 26, Created)

```

DT	01-Jul-1993 (Rel. 26, Last sequence update)
DT	16-Oct-2001 (Rel. 40, Last annotation update)
DE	ADP, ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT3).
DE	SLC25A6 OR ANT3.
OS	Bos taurus (Bovine).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC	Bovidae; Bovinae; Bos.
OX	NCBI_TaxID:9913;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE:69229093; PubMed:2540808;
RA	Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT	"Two bovine genes for mitochondrial ADP/ATP translocase expressed differences in various tissues.";
RL	Biochemistry 28:866-873(1989).
CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC	-1- SUBUNIT: HOMODIMER.
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC	-----
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CC	-----
DR	EMBL: M24103; AAA30769.1; .
DR	PIR: B43646; B43646.
DR	InterPro: IPR002067; mt_carrier.
DR	InterPro: IPR001993; Mitoch_carrier.
DR	Pfam: PF00153; mito_carri; 3
DR	PRINTS: PR00926; MITOCARRIER.
DR	PROSITE: PS00215; MITOCH_CARRIER; 3.
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; Multigene family.
FT	TRANSMEM 12..29 1 (POTENTIAL).
FT	TRANSMEM 73..91 2 (POTENTIAL).
FT	TRANSMEM 117..134 3 (POTENTIAL).
FT	TRANSMEM 176..195 4 (POTENTIAL).
FT	TRANSMEM 214..231 5 (POTENTIAL).
FT	TRANSMEM 273..291 6 (POTENTIAL).
FT	REPEAT 2..111 1.
FT	REPEAT 112..208 2.
FT	REPEAT 209..298 3.
SQ	SEQUENCE 298 AA: 32877 MW: 134472 DEFEDE4061 CXC64:
Query Match	88.9%; Score 1380.5; DB 1; Length 298;
Best Local Similarity	86.9%; Pred. No. 5,1e-119;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1.	
OY	1 MGDHANSLKDFLGLGAVAAANAKRVNAPAEIVKLLLOVCHANSKOTSAKOYKGIIDCVR 60
DB	1 MTEOAIISFAKQFLGAGIAAIAKSTAVAPAEIVKLLLOVCHANSKOTLAADOKYGVDCIVR 60
OY	1 PRKQGLSPFRGNLANVIRYFPQALAFKADKYKQLFAGVDRNKOFRNRYFAGNLASG 120
DB	61 IPKQGVLSLFRGNLANVIRKFPQALNFAKDKYKQLFAGVDRNKOFRNRYFAGNLASG 120
OY	121 GAAGATSLCEFYVPLDFARTLADVGR-AQREFHGLDCSTIKKIFKSDGLNGLYOGFNVS 179
DB	121 GAAGATSLCEFYVPLDFARTLADVGR-AQREFHGLDCSTIKKIFKSDGLNGLYOGFNVS 180
OY	180 VGGIITRAAFVGVYDRAKGLRPKNVHIVSMILQSNVAVAGLSYPRDVARRRMM 239
DB	181 VGGIITRAAFVGVYDRAKGLRPKNVHIVSMILQSNVAVAGLSYPRDVARRRMM 240

RESULT 11

ADT_ANOGA STANDARD: PRT: 301 AA.

AC Q27238:

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).

OS Anopheles gambiae (African malaria mosquito).

OC Eukaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda: Insecta: Pterygota: Neoptera: Endopterygota: Diptera: Nematocera: Culicoidae: Anopheles.

OC NCBI_TaxID=7165;

OX NCBI_TaxID=7165;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=G3:

RX MEDLINE=94348635; PubMed=8069414;

RA Beard C.B., Crews-Oyen A.E., Kumar V.K., Collins F.H.:

RT "A cDNA encoding an ADP/ATP carrier from the mosquito *Anopheles gambiae*."

RL Insect Mol. Biol. 3:35-40(1994).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

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CC -----

CC EMBL: L11618; AAB04104.1; -

DR EMBL: L11617; AAB04105.1; -

DR InterPro: IPR002067; Mit_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 14 31 1 (POTENTIAL).

FT TRANSMEM 75 93 2 (POTENTIAL).

FT TRANSMEM 119 136 3 (POTENTIAL).

FT TRANSMEM 178 197 4 (POTENTIAL).

FT TRANSMEM 216 233 5 (POTENTIAL).

FT TRANSMEM 275 293 6 (POTENTIAL).

SO SEQUENCE 301 AA; 32863 MW; 4CC9E17C9F8DA08B CRC64;

Query Match 74.9%; Score 1162.5; DB 1; Length 301;

Best Local Similarity 76.9%; Pred. No. 4.5e-99;

Matches 223; Conservative 26; Mismatches 40; Indels 1; Gaps 1;

OY 6 WSFLKDLFLAGAAVAASKTAVAPIERVKLLLOVOHASQOISAEK--QYKGIIDCVRIPEQ 65

DB 8 YGFAPKDLFLAGISAAVSTKTAVAPIERVKLLLOVOHASQOISAEKQIVCFVRIPEQ 67

OY 66 GFLSPWRCNLANVIRPPTOALNFAFKDKYKQLFLGVDYRRHKQFRRYFAGNLASGGA 125

DB 68 GIGAFWRCNLANVIRPPTOALNFAFKDKYKQVFLGVDYRRHKQFRRYFAGNLASGGA 127

OY 126 TSLCFVYPLDFAFRLADVGRRRA-QREFHGLGDCIIFKSDGLRGLYGCFNVSOGII 184

DB 128 TSLCFVYPLDFAFRLADVGRRRA-QREFHGLGDCIIFKSDGLRGLYGCFNVSOGII 187

OY 185 IYRAAYFGVYDTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTPFDTVRRRMMQSGRK 244

RESULT 12

ADT_CHLKE STANDARD: PRT: 339 AA.

AC P31692:

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).

OS Chlorella kessleri.

OC Eukaryota: Viridiplantae: Chlorophyta: Trebouxiophyceae: Chlorellales: Chlorellaceae: Chlorella.

OC NCBI_TaxID=3074;

OX NCBI_TaxID=3074;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=92084708; PubMed=1748677;

RA Hilgath C., Sauer N., Tanner W.:

RT "Glucose increases the expression of the ATP/ADP translocator and the glyceraldehyde-3-phosphate dehydrogenase genes in *Chlorella*."

RL J. Biol. Chem. 266:24044-24047(1991).

CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC -----

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CC -----

CC EMBL: M76669; AAA33027.1; -

DR PIR: A41677; A41677.

DR InterPro: IPR002067; Mit_carrier.

DR InterPro: IPR001993; Mitoch_carrier.

DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.

FT TRANSMEM 45 62 1 (POTENTIAL).

FT TRANSMEM 108 126 2 (POTENTIAL).

FT TRANSMEM 151 168 3 (POTENTIAL).

FT TRANSMEM 209 228 4 (POTENTIAL).

FT TRANSMEM 248 265 5 (POTENTIAL).

FT TRANSMEM 304 322 6 (POTENTIAL).

SO SEQUENCE 339 AA; 36686 MW; 54779734A33B3942 CRC64;

Query Match 62.7%; Score 973.5; DB 1; Length 339;

Best Local Similarity 65.3%; Pred. No. 1e-81;

Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

OY 7 SFLKDLFLAGAAVAASKTAVAPIERVKLLLOVOHASQOISAEK--QYKGIIDCVRIPEQ 64

DB 40 AFVADLLAGTAGAIASTAVAPIERVKLLLOVOHASQOISAEKQIVCFVRIPEQ 99

OY 65 QGFLSPWRCNLANVIRPPTOALNFAFKDKYKQLFLGVDYRRHKQFRRYFAGNLASGGA 124

DB 100 QGVAFWRCNLANVIRPPTOALNFAFKDKYKQLFLGVDYRRHKQFRRYFAGNLASGGA 158

OY 125 ATSLCFVYPLDFAFRLADVGRRRA-QREFHGLGDCIIFKSDGLRGLYGCFNVSOGII 184

Dj		11	II	LIIVVPLDLPFATRLAADVGSGSRFEFTGLDCLSSKVRKRGPMALYOGFGVSOCII	218
Dk	159	AGSLTIIVPLDLPFATRLAADVGSGSRFEFTGLDCLSSKVRKRGPMALYOGFGVSOCII	218		
Dl	185	IYRAAYPCVYTARTGML-PDDKNVHIFPSMIIAOSVTAVACLLSPPTPTVRRRMNOSGR	243		
Dm	219	VYRGVYFCPLYDTAGVLGFKKDERJTAFFFKMAVAQAVLVTAAGCVLSLPTFYRRLIMOS--	276		
Dn	244	KGADIMTYGTVDCKRIAKDECAKAFFEGANSNVLRGCGAFVFLVLEIKKYV	297		
Do	277	-GGEOYVNGTIDCKNRKVAQOQGMAFFGCANSNVLRGAGCAFVLVLVEIKKI	329		
<hr/>					
RESULT 13					
ID	ADT_CHLRE	STANDARD:	PRT:	308 AA.	
AC	P27080:				
Dt	01-AUG-1992	(Rel. 23, Created)			
Dt	01-AUG-1992	(Rel. 23, Last sequence update)			
Dt	01-OCT-1994	(Rel. 30, Last annotation update)			
De	ADP_ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).				
CN	ABT.				
Os	Chlamydomonas reinhardtii.				
Oc	Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;				
Ox	Chlamydomonadaceae; Chlamydomonas.				
RN	NCBI_TaxID=3055;				
RP	SEQUENCE FROM N.A.				
RX	STRAIN=FUD44-R2;				
RZ	MEDLINE=93204887; PubMed=8455552;				
RA	Sharpe J.A., Day A.:				
RT	"Structure, evolution and expression of the mitochondrial ADP/ATP translocator gene from Chlamydomonas reinhardtii."				
RL	MoJ. Gen. Genet. 237:134-144(1993).				
CC	-1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.				
CC	-1 SUBUNIT: HOMODIMER.				
CC	-1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.				
CC	-1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	-1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL: X65194; GAA46311.1; -				
CC	PIR: S30259; S30259.				
DR	InterPro: IPR002067; Mlt_carrier.				
DR	InterPro: IPR001993; Mitoch_carrier.				
DR	Pfam: PF00153; mltc_carrf. 3.				
DR	PRINTS: PR00926; MITOCARRIER.				
DR	PROSITE: PS00215; MITOCH_CARRIER. 2.				
KW	Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.				
FT	TRANSMEM 12 .. 29 1 (POTENTIAL).				
FT	TRANSMEM 74 .. 92 2 (POTENTIAL).				
FT	TRANSMEM 116 .. 133 3 (POTENTIAL).				
FT	TRANSMEM 178 .. 197 4 (POTENTIAL).				
FT	TRANSMEM 217 .. 234 5 (POTENTIAL).				
FT	TRANSMEM 273 .. 291 6 (POTENTIAL).				
SO	SEQUENCE 308 AA; 33528 MW; DA77CF0E72B7A53F CMC64;				
<hr/>					
Qy	Query Match	49.6%;	Score 770..5;	DB 1;	Length 308;
	Best Local Similarity	52.6%;	Prod. No. 3.4e-63;		
	Matches 159;	Conservative 49;	Mismatches 77;	Indels 17;	Gaps 6;
<hr/>					
Dy	7	SFLADFLAGAANAASKTAAPIERVKLLLOVO-HASKQISAEKOYKICDCVRIPEPO	65		
Dz	7	NPNVDVLGGISAASVSKTAAPIDIEVKLLIIONDOEMIKGRLASIPYKIGECFVRTAAEE	66		

ID	ADT1	MAIZE	STANDARD	PRT	387	AA
OY	66	GLSLPGRNGLNVIVITPPQALNFPKQYKQQLFGVGRDRIHQFRRYFAGNLASGAGA	125			
Db	67	CGSLIMRNTANVIVITPPQALNFPKQYKQQLFGVGRDRIHQFRRYFAGNLASGAGA	124			
OY	126	TSLSCEVYLPDAPARTRLAADVGR---AOREFHGLGDC11K1FKSDGLRGLYOCFNVSVQ	181			
Db	125	VSLSFVSLDYAPARTRLANDAKSAAKGGDGRQNLVDYVRKRTIASDGIAGLYRGFNISCV	184			
OY	182	G111YRAAYFCGYDTRAKG-MLPDPKNNVH1EVSWM1AQSVTAVAGLLSTPFDTVRRRRMMQ	240			
Db	185	G11YVYRGLYFCGMYSDSLKPVLVGLVGLPANNFLAFLGLGMGITIGAGLASVP1DIT1RRRMHT	244			
OY	241	SGRGADIMYGTGYDCMRKIKKDECAKAPFGAGSNVLRGMGAPVLVLYDE1-----K	294			
Db	245	S---GSAVKYNSFFHCFOEIVKNBCGMSLFGAGANILRAVAGAVLGLGYDLOY1LLGK	301			
OY	295	KY 296				
Db	302	KY 303				
RESULT 14						
ADT1	ADT1	MAIZE	STANDARD	PRT	387	AA
AC	AC	ADT1	MAIZE	STANDARD	PRT	387
AC	AC	ADT1	MAIZE	STANDARD	PRT	387
DT	DT	13-AUG-1987	(Rel. 05, Created)			
DT	DT	01-AUG-1992	(Rel. 23, Last sequence update)			
DT	DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	DE	ADP,ATP carrier protein 1, mitochondrial precursor (ADP/ATP				
DE	DE	translocase 1) (Adenine nucleotide translocator 1) (ANT 1).				
CN	CN	ANT1 OR ANT-G1.				
OS	OS	Zea mays (Maize).				
OC	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;				
OC	OC	Panicoidae; Andropogoneae; Zea.				
OX	OX	NCBI_TaxID=4577;				
RP	RP	11				
RC	RC	SEQUENCE FROM N.A.				
RC	RC	STRAIN=MUTIND-FR7205034;				
RA	RA	MEDLINE=91322533; PubMed=1863785;				
RA	RA	Winding B.M., Day C.D., Sarah C.J., Leaver C.J.;				
RT	RT	"Nucleotide sequence of two cDNAs encoding the adenine nucleotide				
RT	RT	translocator from Zea mays L.";				
RL	RL	Plant Mol. Biol. 17:305-307(1991).				
RN	RN	12				
RP	RP	SEQUENCE OF 59-387 FROM N.A.				
RC	RC	STRAIN=CV. B37N;				
RC	RC	MEDLINE=89338399; PubMed=2547608;				
RA	RA	Leaver C.J., Bathgate B., Baker A.;				
RA	RA	"Two genes encode the adenine nucleotide translocator of maize				
RT	RT	mitochondria. Isolation, characterisation and expression of the				
RT	RT	structural genes.";				
RL	RL	Eur. J. Biochem. 183:303-310(1989).				
RN	RN	13				
RP	RP	SEQUENCE OF 70-387 FROM N.A.				
RC	RC	MEDLINE=85297781; PubMed=2994015;				
RA	RA	Baker A., Leaver C.J.;				
RA	RA	"Isolation and sequence analysis of a cDNA encoding the ATP/ADP				
RT	RT	translocator of Zea mays L.";				
RL	RL	Nucleic Acids Res. 13:5857-5867(1985).				
CC	CC	-1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE				
CC	CC	MITOCHONDRIAL INNER MEMBRANE.				
CC	CC	-1- SUBUNIT: HOMODIMER.				
CC	CC	-1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial				
CC	CC	inner membrane.				
CC	CC	-1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.				
CC	CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.				
CC	CC	-----				
CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation				
CC	CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	CC	use by non-profit institutions as long as its content is in no way				

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CC EMBL: X57556; CA40781.1; -
 CC EMBL: X15711; CA33742.1; -
 CC EMBL: X02842; CA26600.1; -
 CC PIR: A24072; A24072.
 CC PIR: S05199; S05199.
 CC PIR: S14876; S14876.
 CC MaltEDB: 17145; -
 CC InterPro: IPR002067; Mit_carrier.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr; 3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER; 2.
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC Transmembrane; Multigene family.
 CC TRANSIT 1 77 MITOCHONDRION.
 CC CHAIN 1 77 ADP-ATP CARRIER PROTEIN 1.
 CC TRANSMEM 78 387 1 (POTENTIAL).
 CC TRANSMEM 91 108 2 (POTENTIAL).
 CC TRANSMEM 153 171 3 (POTENTIAL).
 CC TRANSMEM 196 213 4 (POTENTIAL).
 CC TRANSMEM 257 276 5 (POTENTIAL).
 CC TRANSMEM 296 313 6 (POTENTIAL).
 CC TRANSMEM 352 370 6 (POTENTIAL).
 CC TRANSMEM 102 102 K -> E (IN REF. 2).
 CC TRANSMEM 154 154 N -> Y (IN REF. 3).
 CC CONFLICT 154 154
 CC SEQUENCE 387 AA; 42391 MW; DE73B80F478BD57D CRC64;

Query Match 48.7%; Score 756.5; DB 1; Length 387;
 Best Local Similarity 53.8%; Pred. No. 8.4e-62;
 Matches 164; Conservative 41; Mismatches 77; Indels 23; Gaps 7;

OY 7 SFLDPLAGAAVAVSKTAVPIERVKLLQVO-HASKOISAEKQYKIIDCVVRIPEQ 65
 DB 86 NPMIDFMGWSAASVSKTAAPIERVKLLQVODEMIKSGRLSEYKIVDCFRITKDE 145
 OY 66 GFLSPWRCNLAVNIRPEPTQALNFAFKDYKQOLGCVDRHKQFRRFAGNLASGGA 125
 DB 146 GFSLSMRGNTANVIRPEPTQALNFAFKDYKQOLGCVDRHKQFRRFAGNLASGGA 204
 OY 126 TSLCFVYPLDFARTRLADVGR--AOREFHGLGDCIYKIFKSDGLRGLYOGFNVSG 182
 DB 205 SSLPFVYSLDARRLANDAKAAGCGGROFNLVDYRKTLKSDGLRGFVJSCVG 264
 OY 183 IIVRAAFGVYDTAK-----GMLPDPKVNHI FVSMIAQSVTAVAGLSYPTVRRRM 237
 DB 265 IIVRGILFGLYDSTIKPVLTGNLD----NPFASFLGMLITNGAGLSYPTVRRRM 320
 OY 238 MMOSGRGADIMVTGYDCKWRIAKDEGAKAFKGAWSNVLRGMGAFVLYVDEI--- 293
 DB 321 MMTSGEA---VKYSSLDLAFQOILKKEGPKSLFKGAGANILRAIAGAVLSGYDOLTLF 377
 OY 294 --KKY 296
 DB 378 FGKRY 382

RESULT 15
 ADT_SCHPO STANDARD: PRT: 322 AA.
 ID ADT_SCHPO
 AC 009188;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP-ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 GN ANCI OR SPBC330.10C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.

OX NCBI_TaxID:4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-96257204; PubMed-8675018;
 RA Couzin N., Trezeguet V., Saux A.L., Lauguin G.J.M.;
 RT "Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae."
 RL Gene 171:113-117(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Mablet D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
 RA Skellon J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Roben J., Grymoprez B.,
 RA Wellens J., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerruti L., Lowe T., McCombie M.R., Paulsen I., Polashin J.,
 RA Shpakovskii G.V., Ussery D., Barrett B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

CC EMBL: Z49974; CA90275.1; -
 CC EMBL: AL023634; CA19176.1; -
 CC InterPro: IPR002067; Mit_carrier.
 CC InterPro: IPR001993; Mitoch_carrier.
 CC Pfam: PF00153; mito_carr; 3.
 CC PRINTS: PR00926; MITOCARRIER.
 CC PROSITE: PS00215; MITOCH_CARRIER; 2.
 CC Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 CC TRANSMEM 28 48 1 (POTENTIAL).
 CC TRANSMEM 93 111 2 (POTENTIAL).
 CC TRANSMEM 131 151 3 (POTENTIAL).
 CC TRANSMEM 197 217 4 (POTENTIAL).
 CC TRANSMEM 222 242 5 (POTENTIAL).
 CC TRANSMEM 289 309 6 (POTENTIAL).
 CC SEQUENCE 322 AA; 35020 MW; 8AC3D16A40FA1ARC CRC64;

Query Match 48.5%; Score 752.5; DB 1; Length 322;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2003, 13:31:32 : Search time 80 Seconds
(without alignments)
764.950 Million cell updates/sec

Title: US-09-393-441-31

Perfect score: 1553
Sequence: 1 MGDHANSFLKDFLAGAVAAA.....LRGMCAGFVLVYDEIKKYV 297

Scoring table: BLOSUM62
Gap 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMEL_21:*
2: SP_archaea:*
3: SP_bacteria:*
4: SP_fungi:*
5: SP_human:*
6: SP_invertebrate:*
7: SP_mammal:*
8: SP_mhbc:*
9: SP_organelle:*
10: SP_plant:*
11: SP_rodent:*
12: SP_virus:*
13: SP_vertebrate:*
14: SP_unclassified:*
15: SP_virus:*
16: SP_bacteriophage:*
17: SP_archaeophage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1464.5	94.3	298	6	046373
2	1463.5	94.2	298	11	062164
3	1411.5	90.9	298	6	08SQH5
4	1377.5	88.7	298	13	091YC4
5	1377.5	88.7	298	13	09PRH1
6	1374.5	88.5	298	13	09PRH2
7	1366.5	88.0	298	13	0919M9
8	1245.5	80.2	299	5	095VX4
9	1241.5	79.9	300	5	09NHN5
10	1241.5	79.9	299	5	09SS30
11	1234.5	79.5	317	13	091336
12	1183	76.2	288	5	044093
13	1183	76.2	288	5	044094
14	1147	73.9	307	5	062526
15	1139.5	73.4	304	5	025129
16	1101.5	70.9	315	4	09HOC2

17	1045.5	67.3	313	5	P91410
18	1043.5	67.2	313	5	021103
19	1037.5	66.8	300	5	045865
20	1005.5	64.7	300	5	001813
21	993.5	64.0	300	5	017407
22	989.5	63.7	309	5	097470
23	959	61.8	307	8	09XM22
24	950	61.2	318	5	09B336
25	905.5	58.3	301	5	025692
26	904.5	58.2	301	5	026006
27	841.5	54.2	170	6	09XS69
28	772	49.7	306	5	018683
29	757.5	48.8	305	3	09PM1
30	750.5	48.3	307	5	076286
31	748.5	48.2	303	3	074260
32	746.5	48.1	379	10	049447
33	745.5	48.0	326	5	P91270
34	743.5	47.9	307	5	026697
35	740.5	47.7	366	10	P93767
36	738.5	47.6	388	10	049875
37	731.5	47.1	317	5	09N647
38	728.5	46.9	306	3	P78754
39	727.5	46.8	331	10	041628
40	708	45.6	305	3	09P876
41	705	45.4	305	3	09P875
42	698	44.9	308	3	08TFA7
43	681	43.9	330	10	09FM86
44	676	43.5	298	5	021809
45	659	42.4	262	10	09AVT6

ALIGNMENTS

RESULT 1

046373 ID 046373 PRELIMINARY: PRT: 298 AA.

AC 046373: 01-JUN-1998 (TREMBL) 06, Created)

DT 01-JUN-1998 (TREMBL) 06, Last sequence update)

DT 01-MAR-2002 (TREMBL) 20, Last annotation update)

DE ADP/ATP translocase.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_Taxid:9986;

RN [1]

RP SEQUENCE FROM N. A.

RC TISSUE=SKLETERAL MUSCLE;

RA Yamaguchi N., Kasai M.

RT "Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle."

RL J. Biochem. 335:541-547(1998).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL

CC -1- INNER MEMBRANE (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.

CC EMBL: AB009386; BAA23777.1; -

CC InterPro: IPR001993; MitochCarrier.

DR InterPro: IPR002067; MitCarrier.

DR Pfam: PF00153; mito_carr; 3.

DR PRINTS: PR00926; MITOCARRIER.

DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Inner membrane; Mitochondrion; Transmembrane; Transport.

SO SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 94.3% Score 1464.5; DB 6; Length 298;

Best Local Similarity 94.6% Pred. No. 6.2e-126;

Matches 282; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGAVAAVSKRAVPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60

DB 1 MSDQALSLKDFLAGVAAVSKRAVPIERVKLLLOVHASKOISAEKQYKGIIDCVR 60

Oy	6	IPKEGGLSPMNGNLNVI	RYEPTALNPAFDKXKOLFGCVDRHKOFRYPAGNLASG	120
Dh	61	IPKEGGLSPMNGNLNVI	RYEPTALNPAFDKXKOLFGCVDRHKOFRYPAGNLASG	120
Oy	121	GAGGATSLCFVYPLPFA	RTPLAADVGR-RAOREFHGLDCCI	179
Dh	121	GAGGATSLCFVYPLPFA	RTPLAADVGR-RAOREFHGLDCCI	179
Oy	121	GAGGATSLCFVYPLPFA	RTPLAADVGR-RAOREFHGLDCCI	179
Dh	121	GAGGATSLCFVYPLPFA	RTPLAADVGR-RAOREFHGLDCCI	179
Oy	180	VGGIITYYRAAYFCGYDTAK	GMLPDPKNVHIIVSWMI	239
Dh	181	VGGIITYYRAAYFCGYDTAK	GMLPDPKNVHIIVSWMI	239
Oy	240	OSGRKADIMYTCTUDCMCK	IAKDKGAKAFRFGASNYLRMGSAFVLVLYDELKXV	297
Dh	241	OSGRKADIMYTCTUDCMCK	IAKDKGAKAFRFGASNYLRMGSAFVLVLYDELKXV	298

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RESULT 2
062164
ID 062164 PRELIMINARY: PRT: 298 AA.
AC 062164;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Adenine nucleotide carrier (Adenine nucleotide translocase 1) (Similar
DE to solute carrier family 25 (Mitochondrial carrier, adenine nucleotide
DE translocator), member 4) (Hypothetical 32.9 kDa protein).
GN SLIC25M4 OR MANC1 OR ANNT1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=MUSCLE;
RA Laplace C.; Costel P.;
RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC Iley S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RA "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes."
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RA Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
RN
RP SEQUENCE FROM N.A.
RC TISSUE=EYE;
RA Strausberg R.;
RA Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (BY SIMILARITY).
CC
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
CC EMBL: X74510; CAA52616.1; -
CC EMBL: AF240002; AAF64470.1; -
CC EMBL: BC003791; AAH03791.1; -
CC EMBL: BC026925; AAH26925.1; -
CC MGD: MGI:1353405; SLIC25M4.
DR InterPro: IPR001993; MitoCh_carrier.
DR InterPro: IPR002067; MLC_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Hypothetical protein; Inner membrane; Repeat; Transmembrane;
KW Transport; Mitochondrion.
KW
SEQUENCE 298 AA: 32904 MW: 34849PEAB0981462 CRC64:

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Query Match	94.28;	Score 1463.5;	DB 11;	Length 298;
Best Local Similarity	94.08;	Pred. No. 7.7e-126;		
Matches 280;	Conservative 10;	Mismatches 7;	Indels 1;	Gaps 1

Qy	1	MDHAAFLDKDLAAGVAAVAAKSTVAAPLERKILLLOVQAHSKOISAEKOYKGI1DCVVR	60
Db	1	MGQALSLFKDLDAAGSLAAVASKTVAAPERKILLLOVQAHSKOISAEKOYKGI1DCVVR	60
Qy	61	1PKEGGFLSPWKGNLANVIARYEPGQALNFAFKDKYKOLFLGVDNRHKOFRYFAGNLASC	120
Db	61	1PKEGGFLSPWKGNLANVIARYEPGQALNFAFKDKYKOLFLGVDNRHKOFRYFAGNLASC	120
Qy	121	GAAGATSLCFVNYPLDFAPTRLAADVGR-RAQREPHGLDLC1IK1FKSGLRLGLVCGFNVS	179
Db	121	GAAGATSLCFVNYPLDFAPTRLAADVGRSSQREPHGLDLC1IK1FKSGLRLGLVCGFNVS	180
Qy	180	VQG111YRAAYFGVYDTAKGMLPDKRNH1IFYSNM1AOSYTAVALGLSLSPDPTVRRRMNM	239
Db	181	VQG111YRAAYFGVYDTAKGMLPDKRNH1IYSNM1AOSYTAVALGLSLSPDPTVRRRMNM	240
Qy	240	QSRKAD1IMYGTLDWCWK1AKDKGAAAFRRGANSNLRMGCAFVLVLDLKKTV	297
Db	241	QSRKAD1IMYGTLDWCWK1AKDKGAANFFRGANSNLRMGCAFVLVLDLKKTV	298

RESULT 3	
08SOH5	
ID 08SOH5	PRELIMINARY; PRT; 298 AA.
AC 08SOH5;	
DT 01-JUN-2002 (Tremblrel, 21, Created)	
DT 01-JUN-2002 (Tremblrel, 21, last sequence update)	
DT 01-JUN-2002 (Tremblrel, 21, last annotation update)	
DE Adenine nucleotide translocator 2.	
OS Bos taurus (Bovine).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;	
OC Bovidae; Bovine; Bos.	
OX NCBI_TaxID=9913;	
RN 11]	
RP SEQUENCE FROM N.A.	
RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;	
RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:	
RT identification of possible amino acids that determine functional	
RT differences in its isoforms.";	
RL Mitochondrion 1:371-379(2002).;	
DR EMBL: AB065433; BAB84673.1; -	
DQ SEQUENCE 298 AA; 32955 MW; C68697BB987879C0 CRC64;	

[illegible]

RESULT 4	
09YIC4	
ID 09YIC4	
PRELIMINARY:	
PRT:	298 AA.

```

AC 09YIC4:
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410:
RN 111
RP MEDLINE=99083429: PubMed=9866197:
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
RT "The origin and differentiation of the heteromorphic sex chromosomes
  2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
  a sex-linked gene, ADP/ATP translocase.";
  Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match      88.7%: Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%: Pred. No. 5.7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAVAASKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCVR 60
DB 1 MTDNAISFAKDFLAGVAVAISKTAVAPIERVKLLLOVHASKOITADKOKGIMDCVVR 60
OY 61 IPKEGFLSEFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
DB 61 IPKEGFLSEFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 179
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 180
OY 180 VOGIITRAAFVGYDTAKGMLPDPKKNVHIFVSMIAOSVAVAGLSTPPDYRRRRMM 239
DB 180 VOGIITRAAFVGYDTAKGMLPDPKKNVHIFVSMIAOSVAVAGLSTPPDYRRRRMM 239
OY 240 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYV 297
DB 240 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYV 297
OY 241 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYI 298
DB 241 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYI 298

RESULT 5
O9PRH1 PRELIMINARY: PRT: 298 AA.
ID O9PRH1:
AC O9PRH1:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410:
RN 111
RP MEDLINE=99083429: PubMed=9866197:
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
RT "The origin and differentiation of the heteromorphic sex chromosomes
  2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
  a sex-linked gene, ADP/ATP translocase.";
  Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008457; BAA36507.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

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RT 2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
  a sex-linked gene, ADP/ATP translocase.";
  Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008456; BAA36513.1; -.
DR EMBL: AB008455; BAA36506.1; -.
DR EMBL: AB008461; BAA36511.1; -.
DR EMBL: AB008462; BAA36512.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR Pfam: PF00153; mito_carr. 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match      88.7%: Score 1377.5; DB 13; Length 298;
Best Local Similarity 86.6%: Pred. No. 5.7e-118;
Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGVAVAASKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCVR 60
DB 1 MTDNAISFAKDFLAGVAVAISKTAVAPIERVKLLLOVHASKOITADKOKGIMDCVVR 60
OY 61 IPKEGFLSEFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
DB 61 IPKEGFLSEFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKOFPNRYFAGNLASG 120
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 179
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 179
OY 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AOREFHGLGDCIYKFKSDGLGLYOGFNVS 180
OY 180 VOGIITRAAFVGYDTAKGMLPDPKKNVHIFVSMIAOSVAVAGLSTPPDYRRRRMM 239
DB 180 VOGIITRAAFVGYDTAKGMLPDPKKNVHIFVSMIAOSVAVAGLSTPPDYRRRRMM 239
OY 240 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYV 297
DB 240 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYV 297
OY 241 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYI 298
DB 241 QSGRKGADIMYTGVDCKRIAKDEGAFAFKGAMSNVLRMGCAFVLVYLDEIKKYI 298

RESULT 6
O9PRH2 PRELIMINARY: PRT: 298 AA.
ID O9PRH2:
AC O9PRH2:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
OC Amphibia: Batrachia: Anura: Neobatrachia: Ranioidea: Ranidae: Rana.
OX NCBI_TaxID=8410:
RN 111
RP MEDLINE=99083429: PubMed=9866197:
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.:
RT "The origin and differentiation of the heteromorphic sex chromosomes
  2, W, X, and Y in the frog Rana rugosa, inferred from the sequences of
  a sex-linked gene, ADP/ATP translocase.";
  Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
  INNER MEMBRANE (BY SIMILARITY)
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB008460; BAA36510.1; -.
DR EMBL: AB008458; BAA36508.1; -.
DR EMBL: AB008459; BAA36509.1; -.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mit_carrier.

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DR InterPro: IP002030: Mit. uncoupling.
 DR Pfam: PF00153: mito. carr. 3
 DR PRINTS: PR00926: MITOCARRIER.
 DR PRINTS: PR00784: MTUNCOUPLING.
 DR PROSITE: PS00215: MITOCH_CARRIER, 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 33082 MW: 80225687599406 CRC64:

Query Match 88.5%; Score 1374.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 1.1e-117;
 Matches 257; Conservative 24; Mismatches 16; Indels 1; Gaps 1;

OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 60
 DB 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 60
 OY 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 DB 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 DB 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
 OY 180 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 239
 DB 180 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 239
 DB 181 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 240
 OY 240 OSGRKGADIMYGTVDCKMRKIAKDEGAKAFFGANSNVLRGMGAFVLVLYDEIKKYV 297
 DB 241 OSGRKGADIMYGTVDCKMRKIAKDEGAKAFFGANSNVLRGMGAFVLVLYDEIKKYI 298

RESULT 7
 OY919M9 PRELIMINARY: PRT: 298 AA.
 AC O919M9:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Adenine nucleotide translocase.
 GN ANTI.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 OX NCBI_TaxID=8335;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Crawford M.J., Khosroshahian F., Varmuza S.L., Liversage R.A.;
 RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
 RT Dynamic Patterns of Expression During Development.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 CC INNER MEMBRANE (BY SIMILARITY)
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF231347; AAF63471.1;
 DR InterPro: IP001993; Mitoch_carrier.
 DR InterPro: IP002067; Mit_carrier.
 DR InterPro: IP002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr. 3
 DR PRINTS: PR00926: MITOCARRIER.
 DR PRINTS: PR00784: MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER, 3.
 KW Inner membrane; Mitochondrion; Transmembrane; Transport.
 SQ SEQUENCE 298 AA: 32940 MW: 918740133751877F CRC64:

Query Match 88.0%; Score 1366.5; DB 13; Length 298;
 Best Local Similarity 86.2%; Pred. No. 5.8e-117;
 Matches 257; Conservative 23; Mismatches 17; Indels 1; Gaps 1;
 OY 1 MGDHANSFLKDFLAGVAAVASTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 60
 DB 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 60

DB 1 MTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 60
 OY 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 DB 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 DB 61 IRKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 120
 OY 121 GAAGATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 179
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 180
 OY 180 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 239
 DB 180 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 239
 DB 181 VOGIIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 240
 OY 240 OSGRKGADIMYGTVDCKMRKIAKDEGAKAFFGANSNVLRGMGAFVLVLYDEIKKYV 297
 DB 241 OSGRKGADIMYGTVDCKMRKIAKDEGAKAFFGANSNVLRGMGAFVLVLYDEIKKYI 298

RESULT 8
 OY95VX4 PRELIMINARY: PRT: 299 AA.
 AC O95VX4:
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 OX NCBI_TaxID=62613;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Burnell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 RT rubripes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401758; AAL02100.1;
 DR InterPro: IP001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN 2.
 SQ SEQUENCE 299 AA: 33037 MW: 3C3B8CB2667C3C5E CRC64:

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
 Best Local Similarity 80.3%; Pred. No. 7e-106;
 Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

OY 5 AMSFLKDFLAGVAAVASTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 64
 DB 5 AVSFLKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKHNGIMDCVVR 64
 OY 65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 124
 DB 65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 124
 DB 65 OGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKQFMRYPAGNLASG 124
 OY 125 ATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 183
 DB 125 ATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 184
 DB 125 ATSLCFVYPLDFARTRLAADVGR-ROREFHGLGDCIIKIFKSDGLRGLYOGFNVS 184
 OY 184 IIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 243
 DB 184 IIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 244
 DB 185 IIRYRAAYFGVYDTAKGMLPDPKRVHIFVSMIAQSVTAAGLLSYPTDVRRRMM 244
 OY 244 KGADIMYGTVDCKMRKIAKDEGAKAFFGANSNVLRGMGAFVLVLYDEIKKYV 297
 DB 245 KKAOLLYNTJIDCKMKIYKTEGGAFFFGANSNVLRGMGAFVLVLYDEIKALI 298

RESULT 9
 OY9NHM5 PRELIMINARY: PRT: 300 AA.
 AC O9NHM5:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)

DR InterPro: IPR002067; Mit_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SO SEQUENCE 317 AA; 35005 MW; 5F66B7EBDD5CEB72 CRC64;

Query Match	79.5%	Score 1234.5;	DB 13;	Length 317;
Best Local Similarity	85.7%	Pred. No. 7.6e-105;		
Matches 233; Conservative	21;	Mismatches 17;	Indels 1;	Gaps 1;

[illegible]

RESULT 12			
044093			
ID	044093	PRELIMINARY:	PRT: 288 AA.
AC	044093:		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
D7	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
D7	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	ADP/ATP translocase (Fragment).		
CN	SES.		
OS	Drosophila pseudoobscura (Fruit fly).		
OC	Eukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta:		
OC	Pterygota, Neoptera, Endopterygota, Diptera: Brachycera, Muscomorpha:		
OC	Ephyridioidea: Drosophilidae: Drosophila.		
NCBI_TaxId=7237:			
3X			

1017
 P SEQUENCE FROM N.A.
 P Zeng L.-W., Comerón J.M., Chen B., Kreitman M.;
 A Genetics 0:0-0(1997).
 L
 C -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
 C INNER MEMBRANE (BY SIMILARITY).
 C -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 C EMBL: AF025798; AAB87883.1; -.
 R Flybase: FBgn0023292; Dpse\seeb.
 R InterPro: IPR001993; MitochCarrier.
 R InterPro: IPR002067; MitCarrier.
 R Pfam: PP00153; mito_carr_3.
 R PRINTS: PR00926; MITOCARRIER.
 R PROSITE: PS00215; MITOCH_CARRIER; 3.
 W Inner membrane: Mitochondrion; Repeat; Transmembrane; Transport.
 M NON_TER 288 288
 T SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

	Query Match	Similarity	76.2%	Score 1183;	DB 5;	Length 288;
Best Local				Pred. No. 3.5e-100;		
Matches 226;	Conservative	25;	Mismatches 31;	Indels 2;	Gaps 2;	
Oy	5	AWSLKDFLAGAANAASKTAVAPIERVKLLLOVONASKQISAEKXQYGTIDCVIRPKE	64			
Db	7	AIGVVDKDAAGGISAASVTAVAPIERVKLLLOVONISKSPDQYGVMDCFIRIPIKE	66			
Oy	65	QGLPSFWRCNLNANIYVFRPTDALNFQFADKXKQYLFGLGVNDHKKQFWRFAGNLASGAGAG	124			

Db	67	QGFSSFWRGNLNANIYFPTQALNFARXDYKVOFLGCVGNKQFWMYFNGNLASGCAAG	126
QY	125	ATSLCFYYPIDLPARTRIAAVDYGRRAOREPHGLDPCIIRKPSDGLRGLYOGFNVSVOCII	184
Db	127	ATSLCFYYPIDLPFAATRIAAADTGKGGOREPHGLDNCCLKIRKSDGLVGLVNGFVSVOCII	186
QY	185	IYRAAYFGVVDIAKGMIDPDKNVIIFKSWMIQAOSYTVAVAGLLSPFDYVRRMMOSGRK	244
Db	187	IYRAAYFGVVDIAK-MIDPDKNPIIYSAIQAQVYTVAVGI VSPFDYVRRMMOSGRK	245
QY	245	GADIMYGTGVDCKRIKADGCAAFKFGAMSNVLRGCGAFVLY	288
Db	246	ATEIITYKNTLHCMAITIAKOGCS-AIFKFGAASNVLRGTGCGAFVLY	288

RESULT 13			
ID	044094	PRELIMINARY:	PRT: 288 AA.
AC	044094;		
DT	01-JUN-1998 (TREMBLrel. 06, Created)		
DT	01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE	ADP/ATP translocase (Fragment).		
GN	SESB.		
OS	Drosophila subobscura (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7241;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;		
RL	Genetica 0:0-0(1997).		
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL		
CC	INNER MEMBRANE (BY SIMILARITY).		
CC	-1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.		
DR	EMBL: AF025799; AAB87884.1;...		
DR	FLYbase: FBgn0023237; Dsub/seSB.		
DR	InterPro: IPR001993; Mitoch_carrier.		
DR	InterPro: IPR002067; MLC_carrier.		
DR	Pfam: PF00153; mito_carf. 3.		
DR	PRINTS: PR00926; MITOCARRIER.		
DR	PROSITE: PS00215; MITOCH_CARRIER. 3.		
KW	Inner membrane; Mitochondion; Repeat; Transmembrane; Transport.		
FT	NOI_ter 288		
EQ	SEQUENCE 288 AA: 31775 MW: 06A1D1E477E81B26 CRC64:		

	Query Match	76.28;	Score 1183;	DB 5;	Length 288;
	Best Local Similarity	79.68;	Pred. No. 3.5e-100;		
	Matches 226;	Conservative 23;	Mismatches 33;	Indels 2;	Gaps 2;
OY	5 AMSFLKDFLGAATAAAVSKTAVAPIEPIVKLLLOVOHAKSOISAEKOYKGIIIDCVRIPE	64			
DQ	7 AMGVNDFAAGGISAASKTAVAPIERVKLLLOVOHI SKOISPDKOKGVDCFIPIAPE	66			
OY	65 QGFLEFRCGLNAVIVIRFPQALNPAFKDXYKQLPLFGVDYRHKOFNRIFAGNLASGAAG	124			
DQ	67 QGFSSFRKGLNAVIVIRFPQALNPAFKDXYKYOVPLFGVDYKNQPHRYFMGNLASGAAG	126			
OY	125 ATSLCFVYPLDPARTRLADVGRRARREFHLGDCLIKFSKSDGLGLYOGFNVSVOGI	184			
DQ	127 ATSLCFVYPLDPARTRLADVTGGKGRFEFLGNCILTKIFKSGLVLGYRGFVSVSGI	186			
OY	185 IYRAATFGVVDITAKGMLPDPKNVHIFVSMIAIOSVTAVAGLSLPEDTVRRRMMSGRK	244			
DQ	187 IYRAAAYFGFYDIAR-MLPDKNTPIYISMIAIOCTVTVAIGVSPEDTVRRRMMSGRK	245			
OY	245 GADIMYTGVDICWRKIATKDGAKAFFPKGAANSNLRMGCAFVLY	288			
DQ	246 ATELIYKNTIHCMGTIAKQEGT-AFFKRGAASNLRMGCAFVLY	288			

OY	5	AMSLKPLFLGAAVAAASKPAVPIEIVKLLLOVHASKOISAEKOYKGIIDCVRIPIE	64
		I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I	
Db	7	AMGFVADPFAAGIGISAASKTAAPRIEYKLLLOVOHISKOISPDKOYKGVDFIPIPE	66
OY	65	OGFLSPWKGMLANVIKYPPTQALNPAFKDKYKQFLGVDNRHKQFMRYPAGNLASGGA	124
		I I I I I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I	
Db	67	OGESSEFMRGMLANVIKYPPTQALNPAFKDKYKQFLGVDNKQFMRYPAGNLASGGA	126
OY	125	ATSLCFVYPLDPFATRIPLAADVGRRAQREFHGLDCLIKIFKSGGLGVLQGFVSVQGI	184
		I I I I I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I	
Db	127	ATSLCFVYPLDPFATRIPLAADVGRRAQREFHGLDCLIKIFKSGGLGVLQGFVSVQGI	186
OY	185	IYRAAVFGVVDTRAKGMLPDPKANHIFVSNMIAQSVTAAGLSLSPEDTVRRRMMQSGR	244
		I I I I I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I	
Db	187	IYRAAVFGVVDTRAKGMLPDPKANHIFVSNMIAQSVTAAGLSLSPEDTVRRRMMQSGR	245
OY	245	GADIMYTGVDCAKRIKAKDEGAKAFKGAANSVLRGMCAGFVLV	288
		I I I I I : I I I I I : I I I I I : I I I I I : I I I I I : I I I I I	
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AC 062526:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE AN72 protein
CN AN72 OR CCI683.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
CC Cyclorhiza; Drosophilidae; Drosophila.
CX NCBI_Taxid=7227;
EN 111
FP SEQUENCE FROM N.A.
FC STRAIN=BERKELEY;
FX MEDLINE=20196006; PubMed=10731132;
FA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
FA Amanatides P.G., Scherer S.E., Li P.M., Hoskins R.A., Galie R.F.,
FA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
FA Sultón G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
FA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champé M., Pfeiffer B.D.,
FA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
FA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
FA Bailei R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
FA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
FA Borrova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
FA Burks K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra J.,
FA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
FA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
FA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
FA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
FA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
FA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
FA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
FA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
FA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
FA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
FA Lasro P., Lei Y., Levitsky A.C., Li J., Li Z., Liang Y., Lin X.,
FA Liu X., Maltsev B., McIntosh T.C., McLeod M.P., McPherson D.,
FA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
FA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
FA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
FA Palczolzi M., Peltman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
FA Reiner K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
FA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
FA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
FA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
FA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
FA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
FA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
FA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT *The genome sequence of Drosophila melanogaster.*;
RL Science 287:2185-2195(2000).
RN 121
RP SEQUENCE FROM N.A.
RC STRAIN=OREGON-R;
RA Zhang Y.O., Davis A.W., Roote J., Ashburner M.;
RL Submitted (MAY-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AEO03484; AAF47956.1; -;
DR EMBL: Y10618; CAA71629.1; -;
DR Flybase: FBgn0025111; Ant2.
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlc_carrier.
DR Pfam: PF00153; mto_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; UNKNOWN_2.
SQ SEQUENCE 307 AA: 33744 MW: 356335D82061C0C CRC64:

Query Match 73.9%; Score 1147; DB 5; Length 307;
Best Local Similarity 73.8%; Pred. No. 7.5e-97;

Matches 214; Conservative 33; Mismatches 43; Indels 7; Gaps 0;
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DB 17 SFLMDFPMGVSAALAKTAVAPAEIEVKLLLOVONHASKOISAEKYGKIIDCVVRIPKEOG 76
QY 67 FLSEFGRNLNANVIRFPPQALNFAFKDKYKOLFSGVDRHKOFPNMFAGNLASGACAT 126
DB 77 FSSFWGRNLNANVIRFPPQALNFAFKDKYKOLFSGVDRHKOFPNMFAGNLASGACAT 136
QY 127 SLCFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDLRLYOGFNVSVGCI11Y 186
DB 137 SLCFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDLRLYOGFNVSVGCI11Y 196
QY 187 RAAFGVYDTAKGLPDDKNVIFVSMIAOSVTVAVAGLLSPPTVRRRMMNOSGRCA 246
DB 197 RAAFGVYDTAKGLPDDKNVIFVSMIAOSVTVAVAGLLSPPTVRRRMMNOSGRCA 256
QY 247 DMYNGTYDCMKRIKDEGAKAFKFGAMSVNLVGRGAFVLVLYDEIKKY 296
DB 257 EMVYNTAHCHLVIAKQEGTGAFFKALSNIRGTGALVLYLYDEMKKY 306
RESULT 15
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AC 025129:
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DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE ADP/ATP translocase.
GN HRATLI.
OS Halocynthia roretzi (Sea squirt).
OC Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
OC Stolidobranchia; Pyuridae; Halocynthia.
OX NCBI_Taxid=7729;
RN 111
RP SEQUENCE FROM N.A.
RA Miya T.;
RL Submitted (JAN-1996) to the EMBL/Genbank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RA Miya T., Makabe K., Satoh N.;
RT *Expression of a gene for major mitochondrial protein, ADP/ATP
RT translocase, during embryogenesis in the ascidian Halocynthia
RT roretzi.*;
RL Dev. Growth Differ. 36:39-48(1994).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: D83059; BA11765.1; -;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlc_carrier.
DR Pfam: PF00153; mto_carr.3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Inner membrane; Mitochondrion; Transmembrane; Transport.
SQ SEQUENCE 304 AA: 33307 MW: 51FD0DD7D68634880 CRC64:

Query Match 73.4%; Score 1139.5; DB 5; Length 304;
Best Local Similarity 74.6%; Pred. No. 3.6e-96;
Matches 220; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
QY 6 WS---FLKDFLAGNAVAASKAVAPAEIEVKLLLOVONHASKOISAEKYGKIIDCVVRIP 62
DB 3 WSADVFAKDLAIGTAAAIKSTIVAPAEIEVKLLLOVONHASTOMKAGTEKGIIDAFVRIP 62
QY 63 KEQGFSLFWRGNLANVIRFPPQALNFAFKDKYKOLFSGVDRHKOFPNMFAGNLASGCA 122
DB 63 KEQGFSLFWRGNLANVIRFPPQALNFAFKDKYKOLFSGVDRHKOFPNMFAGNLASGCA 122
QY 123 AGATSLCFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDLRLYOGFNVSVG 182
DB 123 AGATSLCFVYPLDFARTRLAADVGRRAOREFHQGLDCIIRKFSQDLRLYOGFNVSVG 182

Db	123	AGATGLCFVYPLDFARTRLADIGSGSRQFTGLGNCLATIVKKDGPRLYOGFVVSIOG	182
Oy	183	111YRAAYFGVYDTAKGMLPDPKNAHIFVSMIAQSVTAAGLLSPFDIVRRMMQSG	242
Db	183	11YRAAYFGTIDTVKGMPLDPONTP1IVSMIAQVVTGAGIISTYFDFVRRMMQSG	242
Oy	243	RKGADIMYGTVDCAHRIAKDEGAKAFKGAHNSVLRGMGAFVLVLYDEIRKKYV	297
Db	243	RNKEDRMVKGCTVDCMGKIYKNEGKAFKFGALSNVIRGTGALVLYLYDELKKLY	297

Search completed: June 18, 2003, 13:36:01
 Job time : 83 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 02:39:09 : Search time 1656 Seconds

(without alignments)
15711.297 Million cell updates/sec

Title: US-09-393-441-1

Perfect score: 894

Sequence: 1 atgggtatcacgcctggag.....agatcaaaaaatgtctaa 894

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_hlg:*
3: gb_in:*
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5: gb_ov:*
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8: gb_pl:*
9: gb_pt:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vt:*
15: em_da:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vt:*
30: em_hlg_hum:*
31: em_hlg_inv:*
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33: em_hlg_mus:*
34: em_hlg_pln:*
35: em_hlg_rtd:*
36: em_hlg_man:*
37: em_hlg_vrt:*
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39: em_hlggo_hum:*
40: em_hlggo_mus:*
41: em_hlggo_other:*

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Length	DB ID	Description
1	894	100.0	894	AX134718
2	894	100.0	894	AX301846
3	894	100.0	1320	9 HUMTRL
4	873	97.7	1319	9 BC008664
5	794.6	88.9	932	4 AB009386
6	770.6	86.2	1194	4 BOV127315
7	757.8	84.8	1196	6 AX401651
8	757.8	84.8	1196	10 RATANT1
9	751.4	84.0	1070	10 BC026925
10	751.4	84.0	1142	10 BC003791
11	748.2	83.7	1177	10 MMRNANC
12	748.2	83.7	1273	10 MMU27315
13	564.2	63.1	897	6 AX134720
14	564.2	63.1	897	6 AX301848
15	564.2	63.1	1399	9 BC031912
16	562.6	62.9	1193	9 BC008935
17	562.6	62.9	1308	9 BC007295
18	562.6	62.9	1344	9 AY007135
19	562.6	62.9	1366	9 BC007850
20	562.6	62.9	1455	9 BC014775
21	562.6	62.9	1466	9 BC008737
22	561	62.8	1146	4 AB065433
23	561	62.8	1266	5 AF506216
24	558.4	62.5	1349	4 BOV127315
25	554.4	62.0	1289	5 AF231347
26	553	61.9	897	6 AX134719
27	553	61.9	897	6 AX301847
28	553	61.9	897	10 MMU10404
29	553	61.9	1228	9 HUMATPC
30	553	61.9	1236	10 BC004570
31	553	61.9	1244	10 MMU27316
32	553	61.9	1280	10 MMANTAP
33	548.2	61.3	1215	10 RATANT2
34	541	60.5	1308	5 AB008462
35	541	60.5	1315	5 AB008463
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37	539.4	60.3	1318	5 AB008461
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ALIGNMENTS

RESULT 1	AX134718	894 bp	DNA	linear	PAT 29-MAY-2001
LOCUS	AX134718				
DEFINITION	Sequence 1 from Patent WO0132876.				
ACCESSION	AX134718				
VERSION	AX134718.1	GI:14271235			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Murphy/A.N., Cleverger/W., Willey/S.E., Andreyev,A.Y., Frigeri,L.G.,				
TITLE	1 (bases 1 to 894)				
	Velicelcbl.G. and Davis,R.E.				
	Compositions and methods for determining interactions of				

mitochondrial components, and for identifying agents that alter such interactions
Patent: WO 0132876-A 1 10-MAY-2001;

JOURNAL
MITOKOR (US)

FEATURES
Source Location/Qualifiers

1. 894

BASE COUNT 187 a 224 c 267 g 216 t

ORIGIN

Query Match 100.0%; Score 894; DB 6; Length 894;

Best Local Similarity 100.0%; Pred. No. 3.2e-180;

Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

AX301846

LOCUS

DEFINITION

AX301846

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

human.

REFERENCE

AUTHORS

TITLE

JOURNAL

MITOKOR (US)

FEATURES

Source Location/Qualifiers

1. 894

BASE COUNT 187 a 224 c 267 g 216 t

ORIGIN

Query Match 100.0%; Score 894; DB 6; Length 894;

Best Local Similarity 100.0%; Pred. No. 3.2e-180;

Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY      661  GCACTCCGAGGGCTGCTGTCTTACCCCTTTGACACTGTTGCTGTAGATGATGACG 720
Db      661  GCACTCCGAGGGCTGCTGTCTTACCCCTTTGACACTGTTGCTGTAGATGATGACG 720
OY      721  TCCGGCCGGAAGGGCCGATATATGATACAGGGGACAGTTGACTGCTGAGAGAAATT 780
Db      721  TCCGGCCGGAAGGGCCGATATATGATACAGGGGACAGTTGACTGCTGAGAGAAATT 780
OY      781  GCAAAAGACGAAGAGCCAGCCCTTCTTCAAGGTGCTGCTCAATGTCTGAGAGGC 840
Db      781  GCAAAAGACGAAGAGCCAGCCCTTCTTCAAGGTGCTGCTCAATGTCTGAGAGGC 840
OY      841  ATGGCGGCTGCTTTTGTATTTGCTGTGTATGATGATGATCAAAAATATGTCTAA 894
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RESULT 3
LOCUS      HUMTRL      1320 bp      mRNA      linear      PRI 14-JAN-1995
DEFINITION Human mitochondrial ADP/ADP translocator mRNA, complete cds.
ACCESSION J02966
VERSION    J02966.1 GI:339919
KEYWORDS   ADP/ADP translocator.
            Human lower leg muscle, cDNA to mRNA, (library of Okayama-Berg),
            clone pHMANT.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE  1 (bases 1 to 1320)
AUTHORS   Neckelmann, N., Li, K., Wade, R.P., Shuster, R. and Wallace, D.C.
TITLE      cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
            of a leader peptide, divergence from a fibroblast translocator
            cDNA, and coevolution with mitochondrial DNA genes
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 84 (21), 7580-7584 (1987)
MEDLINE    88041149
COMMENT    Draft entry and computer-readable sequence for [1] kindly provided
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            /db_xref="CDB:G00-119-680"
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            VDRHKQFRVRYACNLASGAGATSLCYVPLDPAFTRLADVGRADREFHGLGDCI
            IKIRSDLRGLGCFNVSOGIITIRAYGVDTAGMLPDKNVHIFVSMHTAOS
            VTAAGLSYFDIVRRMMQSGRKADIMYTGTCDCMRKIANDECAKAFKFGAMSN
            VLRMGAGFLVLYLVDIKKYV"
            CDS
            BASE COUNT          341 a      304 c      357 g      318 t
            ORIGIN             102 bp upstream of NcoI site.

Query Match      100.0%      Score 894:      DB 9:      Length 1320:
Best Local Similarity 100.0%      Pred. No. 31e-180:
Matches 894:      Conservative 0:      Mismatches 0:      Indels 0:      Gaps 0:

OY      1  ATGGGTATCAACGCTTGAGAGCTTCTTAAGAGACTTCCTGCGCGGCGGTGCGCCCTGCC 60
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TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villation@bcm.tmc.edu
Villation, D.K., Luna, R.A., Hale, S.M., Huylk, S., Lu, X., Garcia, A.M., Hollway, M., Telford, B., Hodgson, A., Bouck, J., Yu, W., Muzny, D.M., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
Series: IRM Plate: 13 Row: K Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502096.
location/Qualifiers
1. 1319
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/db_xref="taxon:9606"
/clone="MGC:9281 IMAGE:3871960"
/tissue_type="Eye, retinoblastoma"
/clone_lib="NIH-MGC_67"
/lab_host="DH10B"
/note="Vector: pCMV-Sport6"
99..995
/codon_start=1
/product="Unknown (protein for MGC:9281)"
/protein_id="AAH08664.1"
/db_xref="GI:14250454"
/translation="MGDHAASFLKDFLAGVAANAASKTAVAPTEKYLLOVONHASKO
ISAKEYKGIIDCVNIPKEDGFLSKRONLAVIYFPDQANFAFKDYKOLFLGG
VDRHKQFWRVFAFNLAISGAGACATSLCFVYDFATRLADVGKAAQREHGLDC
I1KIFKSDCLRGJYQCFNVSGI1IYRAAYFQVDTAKMLDPKNNVH1FVSMIAO
SVTAVALSVPEPDIVRRMMOSCRKADIMVTGDCMRKIAKDEGAKAFKFGKWS
NVLKMGGAFLVLYDEIKKYY"
BASE COUNT 334 a 302 c 362 g 321 t
ORIGIN
Query Match 97.7%; Score 873; DB 9; Length 1319;
Best Local Similarity 99.1%; Pred. No. 9, 2e-176;
Matches 889; Conservative 0; Mismatches 5; Indels 3; Gaps 1;
OY 1 ATGGGTGATCACCCTTGAGACTTCTTAAGGACTTCTTGCGCGGGCGGTCCGCTGCC 60
|||||
DB 99 ATGGGTGATCACCCTTGAGACTTCTTAAGGACTTCTTGCGCGGGCGGTCCGCTGCC 158
61 GTGTCAAGACCGCGGTCCCGCCCATCGAGAGGCTCAAACTGCTGCTGCAGTCCAGCAT 120
|||||
DB 159 GTGTCAAGACCGCGGTCCCGCCCATCGAGAGGCTCAAACTGCTGCTGCAGTCCAGCAT 218
121 GCCAGCAACAGATCATGCTGAGAGCATTAAGAGCATATTGATTGTGTGTGAGA 180
|||||
DB 219 GCCAGCAACAGATCATGCTGAGAGCATTAAGAGCATATTGATTGTGTGTGAGA 278
OY 181 ATCCCTAAGAGGAGGCTTCTCTCTCTCTGAGAGGCTTAACCTGGCCAACTGATCGT 240
|||||
DB 279 ATCCCTAAGAGGAGGCTTCTCTCTCTCTGAGAGGCTTAACCTGGCCAACTGATCGT 338
241 TACTTCCCAACCAACTCTCAACTTCCCTTTAAGGACAAAGTACAGACGCTTCTTA 300
|||||
DB 339 TACTTCCCAACCAACTCTCAACTTCCCTTTAAGGACAAAGTACAGACGCTTCTTA 398
OY 301 GCGGTGTGATCGGATTAAGCAATTCTGGCGCTACTTGTGTGAACCTGGCGTCCGGT 360

|||||
DB 399 GGGGGTGTGATCGGATTAAGCAAGTCTTGCGGCTACTTGTGTGAACCTGGCGTCCGGT 458
OY 361 GGGGGCGCTGGGGCCCACTCCCTTTCCTTGTCTACCCCTGGACTTTCCTAGACACAG 420
DB 459 GGGGGCGCTGGGGCCCACTCCCTTTCCTTGTCTACCCCTGGACTTTCCTAGACACAG 518
OY 421 TTGGCGTGTGATGTGGCGAGCGG---CGGCCAGCGGATTCATGCTGTGGCGACGT 477
DB 519 TTGGCGTGTGATGTGGCGAGAGGCGCGGCCCAAGCTTTCATGCTGTGGCGACGT 578
OY 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTTACCAGGTTTCAAGCTCT 537
DB 579 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGCGCTTACCAGGTTTCAAGCTCT 638
OY 538 GTTCAAGGATCATATTATCTATAGAGTGGCTTCTACCTTGGAGTATGATACCTCAAGGG 597
DB 639 GTTCAAGGATCATATTATCTATAGAGTGGCTTCTACCTTGGAGTATGATACCTCAAGGG 698
OY 598 ATGCTGCTGACCCCAAGAGAGGTCACATTTTGTGAGCTGGATGATTCGCCAGAGTGT 657
DB 699 ATGCTGCTGACCCCAAGAGAGGTCACATTTTGTGAGCTGGATGATTCGCCAGAGTGT 758
OY 658 ACGGAGTGCAGAGGCTGCTGCTTACCCCTTGTGACACTTTCCTGTGAATGATGATG 717
DB 759 ACGGAGTGCAGAGGCTGCTGCTTACCCCTTGTGACACTTTCCTGTGAATGATGATG 818
OY 718 CAGTCCGGCCCAAGAGGCGCTATATTATGACAGGAGCACTTGTCTGTGAGAGAG 777
DB 819 CAGTCCGGCCCAAGAGGCGCTATATTATGACAGGAGCACTTGTCTGTGAGAGAG 878
OY 778 ATTTGCAAAAGAGCAAGAGGAGCAAGGCTTTCAAAGGTCGCTGCTCAATGTCTGAGA 837
DB 879 ATTTGCAAAAGAGCAAGAGGAGCAAGGCTTTCAAAGGTCGCTGCTCAATGTCTGAGA 938
OY 838 GGCATGCGCGGTCTTCTTATGTTGTTGATGATGATGATCAAAAATATGCTTAA 894
DB 939 GGCATGCGCGGTCTTCTTATGTTGTTGATGATGATGATGATCAAAAATATGCTTAA 995
RESULT 5 932 bp mRNA linear MM 13-FEB-1999
LOCUS AB009386
DEFINITION Oryctolagus cuniculus mRNA for Adp/ATP translocase, complete cds.
ACCESSION AB009386
VERSION AB009386.1 GI:2668411
KEYWORDS ADP/ATP translocase.
SOURCE Oryctolagus cuniculus neonate male skeletal muscle cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (sites)
AUTHORS Yamaguchi, N. and Kasai, M.
TITLE Identification of a 30kDa calsequestrin-binding protein, which regulates calcium release from sarcoplasmic reticulum of rabbit skeletal muscle
JOURNAL 1. Biochem. 335, 541-547 (1998)
REFERENCE 2 (bases 1 to 932)
AUTHORS Yamaguchi, N. and Kasai, M.
TITLE Direct Submission
JOURNAL Submitted (02-DEC-1997) Naohiro Yamaguchi, Osaka University, Division of Biophysical Engineering, Machikaneyama 1-3, Toyonaka, Osaka 560, Japan (E-mail: n.yam@bpe.es.osaka-u.ac.jp, Tel: +81-6-850-6542, Fax: +81-6-850-6557)
FEATURES
source
1..932
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/db_xref="taxon:9986"
/sex="male"
/tissue_type="skeletal muscle"
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14..910
/codon_start=1

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ISAEKQYKGIIDCVVRIPEEGFLSPFNGNLANYIRPEPTOLNFAFDKXKQIFLG
VDRHKOFMRYPFAGNLASGAAGATSLCEVYPLDFAIRLADVKGAOEFSGLGNC
LTKIFKSDGLRGLYOGFNVSOGIILIRAAVFGYDTRAKGLPPKRVNHIIVSMHIO
TVAVAGLVSYPEDTVRRMMOSGRKADIMYGTVDCKMKIAKDEGKAFFGANS
NVLKMGCAFVLYDEIKKVV"
BASE COUNT      198 a      235 c      275 g      224 t
ORIGIN

Query Match      88.9%: Score 794.6; DB 4; Length 932;
Best Local Similarity 93.6%: Pred. No. 4.7e-159;
Matches 840; Conservative 0; Mismatches 54; Indels 3; Gaps 1;

OY 1 ATGGGTGATCACGCTTGAGAGCTTCTTAAGAGCTTCGCGCGGCGGCTGCCGCTCC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 14 ATGAGTGTATCAGGCTTGAGAGCTTCTTAAGAGCTTCTGCGAGGCTGCCGCTCC 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 61 GTCTCCAGACCGCGCTGCCGCCATGAGAGGCTCAAACTGCTGCTCAGTCCAGCAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 74 GTCTCCAGAGCTGCGCTGCCGCCATGAGAGGCTCAAACTGCTGCTCAGTCCAGCAT 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 121 GCCAGCAAGAGATGAGTGTGAGAGAGTAAAGAGGATGATGATGATGATGATGATGA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 134 GCCAGCAAGAGATGAGTGTGAGAGAGTAAAGAGGATGATGATGATGATGATGATGAG 193
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTGAGAGGAGTAACTGGCCCAAGTATCCGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 194 ATCCCAAGAGAGAGGCTTCTCTCTCTCTGAGAGGAGTAACTGGCCCAAGTATCCGT 253
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 241 TACTTCCCAAGAGCTCTCACTGCTCTTCAAGAGACAGTAAAGACAGCTCTTTTA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 254 TACTTCCCAAGAGCTCTCACTGCTCTTCAAGAGACAGTAAAGACAGCTCTTTTA 313
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 301 GGGGGTGTGATCGGCATTAAGAGTCTGGGGCTACTTGTGTTGAACCTGGCGCGCT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 314 GGGGGTGTGATCGGCATTAAGAGTCTGGGGCTACTTGTGTTGAACCTGGCGCGCT 373
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 361 GGGGCGCTGGGGCCACTCCCTTGTCTTGTCTAACCCGCTGAGATTGTGTAGACAGCAG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 374 GGGGCGCTGGGGCCACTCCCTTGTCTTGTCTAACCCGCTGAGATTGTGTAGACAGCAG 433
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 421 TTGGCTGCTGATGTGGCAGCG---CGCCAGCGTGAATTTCATGCTGTGGCGACTGT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 434 TTGGCTGCTGAGTGGCAGCGAGGTCGCCCGAGCGTGAATTTCATGCTGTGGCGACTGT 493
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 478 ATCATCAGATCTTCAAGTGTGATGAGGCTGAGGGGCTCTACAGAGGTTTCAAGCTCTCT 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 494 CTCAACAGATCTTCAAGTGTGATGAGGCTGAGGGGCTCTACAGAGGTTTCAAGTCTCT 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 538 GTCCAGAGCATCATTTATATAGAGCTGCTACTTGGAGTCTATGATGATGATGATGATG 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 554 GTCCAGAGCATCATTTATATAGAGCTGCTACTTGGAGTCTATGATGATGATGATGATG 613
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 598 ATGCTGCTGACCCCAAGAGAGCTGATTTTGTGAGCTGATGATGATGATGATGATG 657
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 614 ATGCTGCTGACCCCAAGAGAGCTGATTTTGTGAGCTGATGATGATGATGATGATG 673
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 658 ACCGAGTGCAGAGGCTGCTGCTTACCCCTTTGACACTGTTGCTGCTGCTGCTGCTGCTGA 717
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 674 ACCGAGTGCAGAGGCTGCTGCTTACCCCTTTGACACTGTTGCTGCTGCTGCTGCTGCTGA 733
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 718 CAGTCCGCGCGGAAAGGCGGATTTATGATACAGGGGAGAGTGTGATGATGATGATGATG 777
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 734 CAGTCCGCGCGGAAAGGCGGATTTATGATACAGGGGAGAGTGTGATGATGATGATGATG 793
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 778 ATTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 794 ATTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 853
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 838 GGCATGGGCGGCTTTTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 894
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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DB 854 GGCATGGGCGGCTTTTGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 910
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 6
BOVTTTRANS
LOCUS      Bovine ADP/ATP translocase T1 mRNA, complete cds.
DEFINITION
VERSION    M24102.1 GI:529414
KEYWORDS   ADP/ATP translocase; translocase.
SOURCE     Bos taurus CDNA to mRNA.
ORGANISM   Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Kuminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
  Powell,S.J., Mead,S.M., Runswick,M.J., and Walker,J.E.
  1 (bases 1 to 1194)
  Two bovine genes for mitochondrial ADP/ATP translocase expressed
  differences in various tissues
  Biochemistry 28 (2), 866-873 (1989)
  MEDLINE 8922903
  PUBMED  2540808
  On Aug 13, 1994 this sequence version replaced gi:341113.
FEATURES
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    location/qualifiers
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        12..908
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          /translation="MSDALSFLKDLPLAGVAAAVSTAVAPIERVKLLLOVHASKO
          ISAEKQYKGIIDCVVRIPEEGFLSPFNGNLANYIRPEPTOLNFAFDKXKQIFLG
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          LTKIFKSDGLRGLYOGFNVSOGIILIRAAVFGYDTRAKGLPPKRVNHIIVSMHIO
          TVAAGLVSYPEDTVRRMMOSGRKADIMYGTVDCKMKIAKDEGKAFFGANS
          NVLKGCAFVLYDEIKKVV"
          1176..1181
            polyA_signal
            polyA_site
  BASE COUNT      298 a      283 c      320 g      293 t
ORIGIN

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Query Match      86.2%: Score 770.6; DB 4; Length 1194;
Best Local Similarity 92.0%: Pred. No. 6e-154;
Matches 825; Conservative 0; Mismatches 69; Indels 3; Gaps 1;

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OY 1 ATGGGTGATCACGCTTGAGAGCTTCTTAAGAGCTTCTGCGCGGCGGCTGCCGCTCC 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 12 ATGAGCGATCAGGCTTGAGAGCTTCTTAAGAGCTTCTGCGCGGCGGCTGCCGCTCC 71
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 61 GTCTCCAGAGAGAGGCTGCCGCCATGAGAGGCTCAAACTGCTGCTGCTGCTGCTGCTGCTGA 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 72 ATCTCCAGAGAGAGGCTGCTGCCGCCATGAGAGGCTCAAACTGCTGCTGCTGCTGCTGCTGA 131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 121 GCCAGCAAGAGATGAGTGTGAGAGAGTAAAGAGGATGATGATGATGATGATGATGATG 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 132 GCCAGCAAGAGATGAGTGTGAGAGAGTAAAGAGGATGATGATGATGATGATGATGATG 191
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTCTCTGAGAGGATTAAGTGGCAAGCTGATCCGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 192 ATCCCAAGAGAGAGGCTTCTCTCTCTCTGAGAGGATTAAGTGGCAAGCTGATCCGT 251
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 241 TACTTCCCAAGAGAGGCTCTCACTGCTCTTCAAGAGAGAGTAAAGAGAGAGAGAGAG 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 252 TACTTCCCAAGAGAGGCTCTCACTGCTCTTCAAGAGAGAGTAAAGAGAGAGAGAGAG 311
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

OY 301 GGGGCTGTGATCGGCATTAAGAGCTTCTGCGCTACTTGTGCTGAACCTGCTGCCGCT 360
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 312 GGGGCTGTGATCGGCATTAAGAGCTTCTGCGCTACTTGTGCTGAACCTGCTGCCGCT 371
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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OY 361 GGGCGCGTGGGGCCACCTCCCTTGTCTCTACCGCGTGCACCTTGGTAGACGAG 420
Lb 372 GGGGACCTGGGGCCACCTCCCTTGTCTCTACCGCGTGCACCTTGGTAGACGAG 431
OY 421 TTGGCTGCTGATGTGGCCAGGCG--CGCCAGCGGTAGTTCATGGTCTGGGAGCTGT 477
Db 432 CTGGCTGCGACGTCGGGCGAAGGTCGCCCGCCAGGGGAGTTCACTGGTCTGGGAGCTGT 491
OY 478 ATCATYCAAGATCTTCAAGTGTGATGGCTGAGGGGGCTTACACAGGCTTTCACAGCTCT 537
Db 492 ATCACCAAGATCTTCAAGTGTGATGGCTGAGGGGGCTTACACAGGCTTTCACAGCTCT 551
OY 538 GTCCAGGATCATATCTATAGAGTCCCTACTTGGAGTCTATGATCTGCGCAAGGCG 597
Db 552 GTCCAGGATCATATCTATAGAGTCCCTACTTGGAGTCTATGATCTGCGCAAGGCG 611
OY 598 ATGCTGCTGACCCCAAGAGTGCACATTTTGTGAGCTGATGATTTGCCACAGTGTG 657
Db 612 ATGCTGCTGACCCCAAGAGTGCACATTTTGTGAGCTGATGATTTGCCACAGTGTG 671
OY 658 ACGGCACTCCGAGGCGTCTGCTTACCCCTTTTGACACTGTCTGTAGATGATGATG 717
Db 672 ACGGCGCTCGGGGGCTGCTGCTTACCCCTTTTGACACTGTCTGTAGATGATGATG 731
OY 718 CAGTCCGCGGGAAGGGCGGATATATGTACACGGGGACAGTGTGCTGTAGATGATG 777
Db 732 CAGTCCGCGGGAAGGGCGGATATATGTACACGGGGACAGTGTGCTGTAGATGATG 791
OY 778 ATTGCACAAGACGAGAGGAGCCCTTCTTCACAGTGTGCTGTAGATGATGATG 837
Db 792 ATTGCACAAGATGAGAGGAGCCCAAGCTTCTTCACAGTGTGCTGTAGATGATGATG 851
OY 838 GGCATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATGATGATGATGATG 894
Db 852 GGCATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATGATGATGATGATG 908

RESULT 7
AX401651 1196 bp DNA linear PAT 06-JUN-2002
LOCUS Sequence 1327 from Patent WO0210453.
AX401651
VERSION AX401651.1 GI:21337831
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 Mendrick, D., Porter, M.W., Johnson, K.R., Castle, A.L. and Elashoff, M.R.
TITLE Molecular toxicology modeling
JOURNAL Patent: WO 0210453-A 1327 07-FEB-2002;
Gene Logic, Inc. (US)
FEATURES
source location/Qualifiers
1..1196
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
/note="EMBL/Genbank Accession No. D12770"
BASE COUNT 295 a 279 c 326 g 296 t

Query Match 84.8%; Score 757.8; DB 6; Length 1196;
Best Local Similarity 91.1%; Pred. No. 3.2e-151;
Matches 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

OY 1 ATGGGTACACCTTGAGACTTCTTAAGACTTCTGCGCGGGCGGCTGCCCTGCC 60
Db 76 ATGGGGATCAGCTTGAGACTTCTTAAGACTTCTGCGAGGTGCGCGCGGCC 135
OY 61 GTCTCAAGACCGCGGCGCCCATGAGAGGTCAAACTGCTGCGCGAGGTCCAGCAT 120
|||||

Db 136 GTCTCAAGACCGCGGTCGCCCATGAGAGGCTCAAACTGCTGCGAGCTCCAGCAT 195
OY 121 GCCAGCAAGACGATCAGTGTGAGACAGTACAAAGGATCATTTGATGTGTGAGA 180
Db 196 GCCAGCAAGACGATCAGTGTGAGACAGTACAAAGGATCATTTGATGTGTGAGA 255
OY 181 ATCCCTAAGACAGGCGTCTCTCTCTTCTGAGAGGGTAACTGCGCAACGTGATCCGT 240
Db 256 ATCCCAAGAGCGCGGCTTCTCTCTCTGAGAGGGTAACTGCGCAACGTGATCCCG 315
OY 241 TACTTCCCAAGCGTCAACTTTCGCTTCAAGGACAGTACAGCACTTCTTTA 300
Db 316 TACTTCCCAAGCGTCAACTTTCGCTTCAAGGACAGTACAGCACTTCTTTA 375
OY 301 GCGGCTGTGATCGGCTTAAGCACTTGTGGCGCTTCTGTGATGATGATGATGATG 360
Db 376 GAGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 435
OY 436 GGGCGACCTGGGGCTTACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 495
Db 421 TTGGCTGCTGATGAGGCGCG--CGCCAGGCTGATGATGATGATGATGATGATG 477
OY 496 CTGGCTGCGACGTCGAGGAGGATCTTCCAGGCTGATGATGATGATGATGATGATG 555
Db 478 ATCATCAAGATCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 537
OY 556 CTCAACAAGATCTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATG 615
Db 538 GTCCAGGATCAT 597
OY 616 GTGAGAGGATCAT 675
Db 598 ATGCTGCTGACCCCAAGAGTGCACATTTTGTGAGCTGATGATGATGATGATGATG 657
OY 676 ATGCTGCTGACCCCAAGAGTGCACATTTTGTGAGCTGATGATGATGATGATGATG 735
Db 658 ACGGCACTCCGAGGCGTCTGCTTACCCCTTTTGACACTGTCTGTAGATGATGATG 717
OY 736 ACAGCGTGGCGGGGCTGCTGCTTACCTTTCACACTGTCTGTAGATGATGATGATG 795
Db 718 CAGTCCGCGGGAAGGGCGCATATATATATATATATATATATATATATATATATAT 777
OY 796 CAGTCCGCGGGAAGGGCGCATATATATATATATATATATATATATATATATATAT 855
Db 778 ATTGCACAAGACGAGAGGAGCCCTTCTTCACAGTGTGCTGTAGATGATGATGATG 837
OY 856 ATTGCACAAGATGAGAGGAGCCCAAGCTTCTTCACAGTGTGCTGTAGATGATGATG 915
Db 838 GGCATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATGATGATGATGATG 894
OY 916 GGCATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATGATGATGATGATG 972
|||||

RESULT 8
RATANT1 1196 bp mRNA linear ROD 28-APR-2000
LOCUS Rattus norvegicus mRNA for mitochondrial adenine nucleotide
DEFINITION translocator.
ACCESSION D12770.1 GI:398592
VERSION D12770.1
KEYWORDS adenine nucleotide translocator; isoform; mitochondrial inner
membrane protein; solute carrier.
SOURCE Rattus norvegicus (strain:Sprague-Dawley) cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 1196)
AUTHORS Shinohara, Y., Kamida, M., Yamazaki, N. and Terada, H.
TITLE Isolation and characterization of cDNA clones and a genomic clone
encoding rat mitochondrial adenine nucleotide translocator

JOURNAL REFERENCE AUTHORS TITLE	JOURNAL MEDLINE REFERENCE AUTHORS TITLE	COMMENT
Biochim. Biophys. Acta 1152 (1), 192-196 (1993)		
94002161		
2 (sites)		
Brandolin, G., Le Saux, A., Trezeguet, V., Lauquin, G.J. and Vignais, P.V.		
Chemical, immunological, enzymatic, and genetic approaches to studying the arrangement of the peptide chain of the ADP/ATP carrier in the mitochondrial membrane		
J. Bioenerg. Biomembr. 25 (5), 459-472 (1993)		
94179128		
3 (bases 1 to 1196)		
Shinohara, Y.		
Direct Submission		
Submitted (03-AUG-1992) Yasuo Shinohara, University of Tokushima, Faculty of Pharmaceutical Sciences: 1 Shomachi, Tokushima, Tokushima 770, Japan (E-mail: yasuoph.tokushima-u.ac.jp, Tel: 81-886-33-7278, Fax: 81-886-33-5196)		
Submitted (03-AUG-1992) to DDBJ by:		
Yasuo Shinohara		
University of Tokushima		
Faculty of Pharmaceutical Sciences		
Tokushima 770		
Japan		
Phone: 0886-31-3111 x6255		
Fax: 0886-33-0510.		
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Best Local Similarity	91.1%:	Pred. No. 3.2e-151;
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0y	121	GGCAGCAAAACAGATCAGTCTGAGAGAGCAGTACAAAGGATCATTGATTGTGCTGAGA 180
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Db	256	ATCCCTAAGAGCAGGGGCTCTCTGCTGAGAGGGGTAACTGCGCCCAACGTATCCGG 315
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Db	316	TACTTCCCAACCAAGCTCTCACTTCGCCCTTCAAGAGCAAGTACAAAGCAGCTTCTT 375
0y	301	GGGGGTGTGATCGGATTAACGACTTCTGGCGGCTACTTGTGTGTTAACCTGGCTCCGGT 360

DB	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	REMARK	COMMENT
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Oy	361	GGGGCCGCTGGGGCCACCCTCCCTTTGCTTTTGTCTACCGCGCTGGACCTTGGTAGACACAGC	420										
Db	436	GGGGCAGCTGGGGCTACTCCCTCTGCTCTCTACCCACACAGCTGGACTTTGGTAGGACACAGC	495										
Oy	421	TTGGCTGCTGATGTGGGCGACGCG--CGCCACGAGCGTGATTCATTTGGCTGGGCGACGCT	477										
Db	496	CTGGCTGCCGACGTGGGACAGGAGATCTTCCAGCGCTGAGTTCAATTGGGCTGGCTGACTCT	555										
Oy	478	ATCATCAAGATCTTCAAGCTGATGGCTGAGGGGGGCTCTACAGAGGTTTCCAAAGCTCTCT	537										
Db	556	CTCACCAAGATCTTCAAGCTGATGGCTGAGGGGCTCTACAGAGGTTTCCAAAGCTCTCTCT	615										
Oy	538	GTCCAAAGCATCATATTATCTATAGAGCTGCTACTTTCGAGCTATGATAGTCCCAAGGGG	597										
Db	616	GTGCAGGCGCATCATCATCTACAGAGCTCCCTACTTCGAGAGCTATGACACTGCCCCAAGGGG	675										
Oy	598	ATGCTGCTGACCCCAAGACGTGCACATTTTGTGAGCTGGATGATTTGCCCAAGAGTGTG	657										
Db	676	ATGCTGCGCAGACCCCAAGAGTGCACATTTTGTGAGCTGGATGATTTGCCCAAGAGTGTG	735										
Oy	658	ACGCGAGTGCAGAGGCGCTGCTGCTCCACCCCTTTTGACACTGTTGCGTGAAGATGATGATG	717										
Db	736	ACAGCCGCTGGCGGGGCTGTGCTCTATCATTTGACACTGCTCCGTCGTAAGATGATGATG	795										
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Db	796	CAGTCTGGCGCGGAAAGGGGCTGATATTATGTACACGGGACAGTTGACTGCTGGAGCAGC	855										
Oy	778	ATTGCAAAAGACGAAGAGCCATTTTCAAGAGCTGCTGCTCCATATGCTGTGAGA	837										
Db	856	ATTGCAAAAGATGAAGAGCAGCAAGACTTTCTTCAAAAGGCTGCTGCTCCAAAGCTGTGAGA	915										
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Db	916	GGCATGGGCGGCGCTTTGTATGCTGTTGTATGATGATGATGATCAAAATAATATGTGTAA	972										
RESULT 9	BC026925	1070 bp	mRNA	linear	ROD 07-AUG-2002								
DEFINITION	Mus musculus, clone MGC:25083 IMAGE:4500784, mRNA, complete cds.												
ACCESSION	BC026925												
VERSION	BC026925.1	GI:20070837											
KEYWORDS	MGC.												
SOURCE	house mouse.												
ORGANISM	Mus musculus												
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.												
AUTHORS	1 (bases 1 to 1070)												
TITLE	Strausberg,R.												
JOURNAL	Direct Submission												
REMARK	Submitted (04-Apr-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Cepher Drive, Room 11A03, Bethesda, MD 20892-2590, USA												
COMMENT	NIH-MGC Project URL: http://mgc.nci.nih.gov												
	Contact: MGC help desk												
	Email: cga@bcm.tmc.edu												
	Tissue Procurement: The Cepko Laboratory												
	cDNA Library Preparation: Life Technologies, Inc.												
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNLI)												


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Oy      778 ATTGCAAAAGAGCAAGAGGAGCCCTTCTTCAAAAGGTGGCTGCTCAATGTGCTAGA 837
Db      867 ATTGCAAAAGATGAAGAGGAGCCAGCCCTTCTTCAAAAGGTGGCTGCTCAATGTGCTAGA 926
Oy      838 GCATGCGCGGTCTTTGTATGTGTTGATGATGATCAAAATAATGTCTAA 894
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RESULT 13
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DEFINITION Sequence 3 from Patent WO0132876.
ACCESSION AX134720
VERSION   AX134720.1 GI:14271237
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
MURPHY,A.N., CLEVELAND,W., WILEY,S.E., ANDREYEV,A.Y., FRIGERI,L.G.,
VEJCELEBI,G. and DAVIS,R.E.
TITILE    Compositions and methods for determining interactions of
           mitochondrial components, and for identifying agents that alter
           such interactions
           Patent: WO 0132876-A 3 10-MAY-2001;
           MITOKOR (US)
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Query Match      63.1%; Score 564.2; DB 6; Length 897;
Best Local Similarity 77.6%; Pred. No. 5.7e-110;
Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

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Db      181 ATCCCAAGAGACAGGCTTCTCTCTTCTGAGAGGGGTAACTGGCCAAAGCTGATCGT 240
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DEFINITION Sequence 3 from Patent WO0185944.
ACCESSION AX301848
VERSION   AX301848.1 GI:17382905
KEYWORDS
SOURCE    human.
ORGANISM  Homo sapiens
REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS  Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
ANDERSON,C.M., DAVIS,R.E., CLEVELAND,W., WILEY,S.E., MILLER,S.W.,
SZABO,T.R., GHOSH,S.S., MOOS,W.H., PEI,Y. and CARROLL,A.K.
TITILE    Production of adenine nucleotide translocator (ant), novel ant
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           Patent: WO 0185944-A 3 15-NOV-2001;
           MITOKOR (US)
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Query Match      63.1%; Score 564.2; DB 6; Length 897;
Best Local Similarity 77.6%; Pred. No. 5.7e-110;
Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Oy      1 ATGGGTATCAACGCTTGGAGCTTCTTAAAGACTTCTGCGGGGCGTCCGCTGCC 60
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Db      841 GGCATGGCGGCGCTTCTGTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 897

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RESULT 15

BC031912

LOCUS BC031912 1399 bp mRNA linear PRI 26 JUN-2002

DEFINITION

Homo sapiens, solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6, clone MGC:29984

IMAGE:5141625, mRNA, complete cds.

ACCESSION BC031912 1399 bp mRNA linear PRI 26 JUN-2002

VERSION BC031912.1 GI:21594692

KEYWORDS

SOURCE MGC.

ORGANISM human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

AUTHORS Strausberg, R.

TITLE Direct Submission

JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

COMMENT Contact: MGC help desk

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>

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Query Match 63.1%; Score 564.2; DB 9; Length 1399;
 Best Local Similarity 77.6%; Pred. No. 5; 5e-110;
 Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

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Db	458	CTGGCAGCGGAGCTGGGAAAGTCAGAGCACAGAGCGCGAGTTCCGACGCGTGGAGACTGC	517
Oy	478	ATCATCAACATCTTCAGTCTGATGTGGCCGTGAGGGGGCGCTACGACGGTTTCCATCTCT	537
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Oy	538	GTCCAAGGCACTATTATCTATAGAGCTGCGTACTTGGGAGCTCTATGATACCTGCCAAAGGG	597
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 2185239 seqs, 112599159 residues

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Listing first 45 summaries

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23: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	894	100.0	894	21 AAD00519 Human adenine nucl
2	894	100.0	894	22 AAS05901 Human adenine nucl
3	894	100.0	894	24 AAS16688 DNA encoding human
4	757.8	84.8	1196	24 ABR63420 Rat sequence diffe
5	746.6	83.3	1259	19 AAV36480 Anti cDNA. Mus sp
6	745	83.3	1177	19 AAV36479 Anti cDNA. Mus sp
7	564.2	63.1	897	21 AAD00521 Human adenine nucl
8	564.2	63.1	897	22 AAS05903 Human adenine nucl
9	564.2	63.1	897	24 AAS16690 DNA encoding human

10	562.6	62.9	1212	22 AA158797 Human polynucleot
11	562.6	62.9	2035	22 AA160583 Human polynucleot
12	553	61.9	897	21 AAD00520 Human adenine nucl
13	553	61.9	897	22 AAS05902 Human adenine nucl
14	553	61.9	897	24 AAS16689 DNA encoding human
15	523.2	58.5	1156	23 AAS91243 DNA encoding novel
16	503.6	56.3	1581	23 ABL18511 Drosophila melanog
17	503.6	56.3	1750	23 ABL20967 Drosophila melanog
18	488	54.6	1116	24 ABR63761 Human cDNA differe
19	488	54.6	1116	24 ABR63761 Gene #2096 used to
20	488	54.6	1116	24 ABR63761 Prostate cancer re
21	473	52.9	5768	24 ABL69347 Colon adenocarcino
22	451.2	50.5	2706	22 AAS29836 Human cytoskeletal
23	451.2	50.5	2706	22 AAS29836 DNA #33 encoding h
24	451.2	50.5	2706	22 AAS29836 Human cDNA differe
25	446	49.9	853	24 ABR64788 Porcine muscular s
26	443.2	49.6	1033	23 AAS61966 Drosophila melanog
27	443.2	48.6	788	24 AAS61967 Porcine muscular s
28	407	45.5	453	22 AAL24495 Human breast cance
29	398.6	44.6	687	24 ABO56282 Human ovarian anti
30	371	41.5	1781	24 AAD33664 Human TRICH-19 cDN
31	362.6	40.6	1251	23 AAS79610 DNA encoding novel
32	346.8	38.8	4545	23 AAS68190 DNA encoding novel
33	330.8	37.0	5407	23 ABL18510 Drosophila melanog
34	330.8	37.0	8031	23 ABL20966 Drosophila melanog
35	292.6	32.7	707	21 AAN01634 Human colon cancer
36	290	32.4	501	24 AAS61620 Lung small cell ca
37	277.8	31.1	943	24 ABR74319 Bovine embryonic g
38	271.8	30.4	520	22 AAL15651 Bovine breast cance
39	249	27.9	988	24 ABR74435 Bovine embryonic g
40	241.6	27.0	464	22 ABA42741 Human breast cell
41	241.6	27.0	464	22 ABA53168 Human foetal liver
42	241.6	27.0	464	22 ABA22942 Probe #1408 for ge
43	241.6	27.0	464	22 AAK01416 Human brain expres
44	241.6	27.0	464	22 AAK26867 Human bone marrow
45	241.6	27.0	464	22 AAL11497 Probe #1430 for ge

ALIGNMENTS

RESULT 1
AAD00519
ID AAD00519 standard; cDNA: 894 BP.
XX
AC AAD00519:
XX
DT 29-AUG-2000 (first entry)
XX
DE Human adenine nucleotide translocator ANTI cDNA. 1*
XX
KW Human; adenine nucleotide translocator; ANTI; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MP; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotrophic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; lactic acidosis; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDO;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome; ss.
XX
OS Homo sapiens.
XX
FH Key
FT 1..894 Location/Qualifiers
FT CDS /*tag= a
FT /product= "ANTI"
XX
XX WO200026370-A2.
XX 11-MAY-2000.
XX

PF 03-NOV-1999; 99WO-US25883.
 PR 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR:
 PI Ghosh SS:
 DR MPI: 2000-365619/31.
 DR P-PSDB: AAV71031.
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Example 1: Page 165; 175pp: English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents to
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
 CC encoding adenine nucleotide translocator ANT1 from human brain.
 XX
 SO Sequence 894 BP; 187 A; 224 C; 267 G; 216 T; 0 other:

Query Match 100.0%; Score 894; DB 21; Length 894;
 Best Local Similarity 100.0%; Pred. No. 2e-248;
 Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGGGTGATACAGCTTGGAGCTTCTTAAGCACTTCTGCGGGGGCGCTGCCCTGCC 60
 DB 1 ATGGGTGATACAGCTTGGAGCTTCTTAAGCACTTCTGCGGGGGCGCTGCCCTGCC 60
 OY 61 GTCTCAAGACCGCGCTGCGCCCATGAGAGGGTCAAACTGCTGCAAGTCCAGCAT 120
 DB 61 GTCTCAAGACCGCGCTGCGCCCATGAGAGGGTCAAACTGCTGCAAGTCCAGCAT 120
 OY 121 GCCAGCAAAAGATCAGTGTGAGAGAGTACAAAGGATCATTTGTTGTGTGAGAGA 180
 DB 121 GCCAGCAAAAGATCAGTGTGAGAGAGTACAAAGGATCATTTGTTGTGTGAGAGA 180
 OY 181 ATCCCTAAGAGAGAGGCTTCTCTCTTCTGAGAGGTTAACTGCGCAACGATCCGT 240
 DB 181 ATCCCTAAGAGAGAGGCTTCTCTCTTCTGAGAGGTTAACTGCGCAACGATCCGT 240
 OY 241 TACTTCCGACCAAGCTCTCAACTTGCCTTCAAGGCAAGTACAAAGCAGCTCTTTTA 300
 DB 241 TACTTCCGACCAAGCTCTCAACTTGCCTTCAAGGCAAGTACAAAGCAGCTCTTTTA 300
 OY 301 GGGGCTGTGATCGGATTAAGAGTCTGAGGCTACTTGTGCTGATTAACCTGCGCTCGGT 360
 DB 301 GGGGCTGTGATCGGATTAAGAGTCTGAGGCTACTTGTGCTGATTAACCTGCGCTCGGT 360
 OY 361 GGGGCTGTGAGGAGGAGCTCCCTTTGCTTTGCTACCGCGCTGAGCTTTGCTAGACGACG 420
 DB 361 GGGGCTGTGAGGAGGAGCTCCCTTTGCTTTGCTACCGCGCTGAGCTTTGCTAGACGACG 420
 OY 421 TTGGCTGTGATGTGGGAGGAGGCGCCAGCGTGATGCTGAGGAGCTGTATC 480
 DB 421 TTGGCTGTGATGTGGGAGGAGGCGCCAGCGTGATGCTGAGGAGCTGTATC 480

DB 421 TTGGCTGTGATGTGGGAGGAGGCGCCAGCGTGATGCTGAGGAGCTGTATC 480
 OY 481 ATCAAGATCTTCAAGTCTGATGCGCTGAGGGGCTCTACAGAGGTTTCAACGCTCTGTC 540
 DB 481 ATCAAGATCTTCAAGTCTGATGCGCTGAGGGGCTCTACAGAGGTTTCAACGCTCTGTC 540
 OY 541 CAAGCATCATTTATCTATAGAGTGGCTACTTGGAGAGCTATGATACGCAAGGGATG 600
 DB 541 CAAGCATCATTTATCTATAGAGTGGCTACTTGGAGAGCTATGATACGCAAGGGATG 600
 OY 601 CTGCTGACCCCAAGAGAGCTGACATTTTGTGAGCTGATGATTTGCCAGAGTGTACG 660
 DB 601 CTGCTGACCCCAAGAGAGCTGACATTTTGTGAGCTGATGATTTGCCAGAGTGTACG 660
 OY 661 GCAGTGCAGGAGGCTGCTGCTCTACCCCTTTCAGACCTGCTGCTGATGATGATGACG 720
 DB 661 GCAGTGCAGGAGGCTGCTGCTCTACCCCTTTCAGACCTGCTGCTGATGATGATGACG 720
 OY 721 TCCGCGCGGAAAGGGCGCATATTTATGACACGGGAGACGTTGACCTGCTGAGCAAGATT 780
 DB 721 TCCGCGCGGAAAGGGCGCATATTTATGACACGGGAGACGTTGACCTGCTGAGCAAGATT 780
 OY 781 GCAAAAGAGAGAGAGGAGGAGGCTTCTTCAAGGCTGCTGCTGCTGAGAGAGC 840
 DB 781 GCAAAAGAGAGAGAGGAGGAGGCTTCTTCAAGGCTGCTGCTGCTGAGAGAGC 840
 OY 841 ATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATCAAAATAATATGCTAA 894
 DB 841 ATGGCGGCTGCTTTTGTATGCTGTTGTATGATGATGATCAAAATAATATGCTAA 894

RESULT 2
 AAS05901
 ID AAS05901 standard: cDNA: 894 BP.
 AC AAS05901:
 XX
 XX
 DT 07-SEP-2001 (first entry)
 XX
 XX
 DE Human adenine nucleotide translocator-1 (ANT-1) cDNA sequence.
 XX
 DE Human: adenine nucleotide translocator-1: ANT-1: MTP; cytochrome b:
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT CDS 1..897
 FT FT /*tag= a
 FT FT /product= "ANT-1"
 XX
 XX MO200132876-A2.
 PD 10-MAY-2001.
 XX
 XX 03-NOV-2000; 2000WO-US30535.
 PF
 XX
 XX 03-NOV-1999; 99US-0434354.
 PR
 XX
 XX (MITO-) MITOKOR.
 PA
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelebi G, Davis RE;
 XX
 XX MPI: 2001-291054/30.
 DR P-PSDB: AAV01198.
 DR
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cytochrome b polypeptide
 PT fused to energy transfer molecule -

XX Disclosure; Fig 1; 186pp; English.

PS

XS

CC The present sequence encodes for human adenine nucleotide translocator-1
CC (ANT-1) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASh sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke.
CC hyperproliferative disorders e.g. cancer, and deafness.

XD Sequence 894 BP; 187 A; 224 C; 267 G; 216 T; 0 other:

Query Match	100.0%:	Score 894:	DB 22:	Length 894:
Best Local Similarity	100.0%:	Pred. No. 2e-248:		
Matches	894:	Conservative	0:	Mismatches 0: Indels 0: Gaps 0:
Oy	1	ATGGGTGATCAACGCTTGAGCGTTCCTTAAGACATCTTGCGCCGGGGCGTCCCGCTGCC	60	
Db	1	ATGGGTGATCAACGCTTGAGCGTTCCTTAAGACATCTTGCGCCGGGGCGTCCCGCTGCC	60	
Oy	61	GTCCTCAAGACCGGGGTGGCCCATCGAGAGGGTCAAACTGCTCTCAGGTCCAGCAT	120	
Db	61	GTCCTCAAGACCGGGGTGGCCCATCGAGAGGGTCAAACTGCTCTCAGGTCCAGCAT	120	
Oy	121	GCACGACAACAGATCAGTCTGAGAGAGCAGTACAAAGGATCATTTGATGTGTGTGAGA	180	
Db	121	GCACGACAACAGATCAGTCTGAGAGAGCAGTACAAAGGATCATTTGATGTGTGTGAGA	180	
Oy	181	ATCCCTAAGAGAGACAGGCTTCTCTCTCTTCTGAGAGGGTAACTGTCGCAAGTATCCGT	240	
Db	181	ATCCCTAAGAGAGACAGGCTTCTCTCTCTCTGAGAGGGTAACTGTCGCAACCTGTATCCGT	240	
Oy	241	TACTTCCACCACCAAGCTCTCACTTCCCTTCAAGAGCAAGTACAAGCAGCTCTTCTTA	300	
Db	241	TACTTCCACCACCAAGCTCTCACTTCCCTTCAAGAGCAAGTACAAGCAGCTCTTCTTA	300	
Oy	301	GGGGGTGTGATCGGCATTAAGCAGTTCTGGCGCTACTTTGCTGTAACTTGCCGTC	360	
Db	301	GGGGGTGTGATCGGCATTAAGCAGTTCTGGCGCTACTTTGCTGTAACTTGCCGTC	360	
Oy	361	GGGGCGCGTGGGGCCACCTCCCTTGGCTTGTCTACCGCGGTGGAATTTGCTAGGACCAAG	420	
Db	361	GGGGCGCGTGGGGCCACCTCCCTTGGCTTGTCTACCGCGGTGGAATTTGCTAGGACCAAG	420	
Oy	421	TTGGCTGCTGATGTGGCGAGCGCGCCAGCGTGAATTCATTTGCTGGCGACGTATC	480	
Db	421	TTGGCTGCTGATGTGGCGAGCGCGCCAGCGTGAATTCATTTGCTGGCGACGTATC	480	
Oy	481	ATCAAGATCTTCAAGTCTGATGGCTGAGAGGGGCTCTACAGAGTTTCAAGTCTCTGTG	540	
Db	481	ATCAAGATCTTCAAGTCTGATGGCTGAGAGGGGCTCTACAGAGTTTCAAGTCTCTGTG	540	
Oy	541	CAAGGCATCATTTATCTATAGAGCTCCTACTTTCGAGAGCTATGATACTGCCAAGGGAGTG	600	
Db	541	CAAGGCATCATTTATCTATAGAGCTCCTACTTTCGAGAGCTATGATACTGCCAAGGGAGTG	600	
Oy	601	CTGCGTACCCCAAGACAGTGCACATTTTGTGAGCTGGATGATTTGCCACAGTGTGAC	660	
Db	601	CTGCGTACCCCAAGACAGTGCACATTTTGTGAGCTGGATGATTTGCCACAGTGTGAC	660	

Oy		661 GCACTCCGAGGGCTGCATGTCCCTACCCCTTTTACACTGTTCGTAGCATATGATCGAG	720
Dd		661 GCAGTGCCAGGGCTGCTGTCTCTACCCCTTTTGACACTGTTCGTAGCATATGATCGAG	720
Oy		721 TCCGCCGCGAAGAAGGGCCGATATTATGTATACACGGGACAGTGTGACTGCTGGAGAGATT	780
Dd		721 TCCGCCGCGAAGAAGGGCCGATATTATGTATACACGGGAGACATTGACTGCTGGAGAGATT	780
Oy		781 GCCAAAGACGACGAGACCAGCCCTTCTTCAAAGTGTGCTGTGCAATGTCTCAGAGCC	840
Dd		781 GCCAAAGACGACGAGACCAGCCCTTCTTCAAAGTGTGCTGTGCAATGTCTCAGAGCC	840
Oy		841 ATGGCGCGGTCTTTTGTATTGTGCTGTGATGATGATGATGCAAAAATAATGTCTAA	894
Dd		841 ATGGCGCGGTCTTTTGTATTGTGCTGTGATGATGATGATGCAAAAATAATGTCTAA	894
RESULT 3			
ID	AAS16688	standard; cDNA: 894 BP.	
XX	AAS16688;		
AC			
XX			
DT	14-FEB-2002	(first entry)	
DE		DNA encoding human adenine nucleotide translocator 1 (ANT1).	
XX			
KW		Human; adenine nucleotide translocator; ANT; ss:	
KW		mitochondrial matrix protein.	
XX		Homo sapiens.	
OS			
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..894	
FT		/tag= a	
FT		/product= "Adenine nucleotide translocator 1 (ANT1)."	
XX			
PN		WO200185944-A2.	
PD		15-NOV-2001.	
XX			
PF		11-MAY-2001; 2001WO-USJ5416.	
XX			
PR		11-MAY-2000; 2000US-0569327.	
PA		(MITO-) MITOKOR.	
P1	Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR,		
P1	Ghosh SS, Moos WH, Pel Y, Carroli AK;		
DR	MP1: 2002-055598/07.		
DR	P-PSDB: AAU10378.		
PT		Novel recombinant expression construct for producing adenine nucleotide	
PT		translocator polypeptides, comprises a regulated promoter linked to	
PT		nucleic acid encoding the polypeptide	
XX			
PS		Example 1: Fig 1; 147pp: English.	
CC		The invention relates to a recombinant expression construct (I)	
CC		comprising a regulated promoter operably linked to a nucleic acid	
CC		encoding an adenine nucleotide translocator (ANT) polypeptide. ANT	
CC		proteins mediate the exchange of ATP synthesised in the mitochondrial	
CC		matrix for ADP in the cytosol. (I) is useful for producing recombinant	
CC		ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and	
CC		culturing the host cell. (I) is also useful for targeting a polypeptide	
CC		of interest to a mitochondrial membrane, where ANT polypeptide is	
CC		expressed as a fusion protein with the polypeptide of interest.	
CC		Recombinant ANT polypeptide, or cells expressing the polypeptide, is	
CC		useful for identifying an agent that binds to an ANT polypeptide. ANT	
CC		ligand is useful for determining the presence of an ANT polypeptide,	
CC		preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating	
CC		ANT from a biological sample, where the ANT ligand is covalently or non-	

Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;

Query Match 84.8% Score 757.8; DB 24; Length 1196;
Best Local Similarity 91.1% Pred. No. 5.8e-209;
Matches 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

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OY 1 ATGGGTATCATCGCTTGGAGCTTCTTAAGAGACTTCTGGCGCGGCGCGCTGCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 76 ATGGGGATCAGAGTTTGAGCTTCTTAAGAGACTTCTGGAGGTCGCGCGCGCC 135

OY 61 GTCTCCAAGACCGCGGTCCGCCATCGAGAGGTCAAACTGTCTGCAAGTCCACAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 GTCTCCAAGACCGCGGTCCGCCATCGAGAGGTCAAACTGTCTGCAAGTCCACAT 195

OY 121 GCCAGCAACAGATCACTGCTGAGAACAGCAGTACAAAGGATCATTTGTTGTGTAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 GCCAGCAACAGATCACTGCTGAGAACAGCAGTACAAAGGATCATTTGTTGTGTAGA 255

OY 181 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGGTAACTGGCCAACTGATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGGTAACTGCGCCAACTGATCCGT 315

OY 241 TACTTCCCAACCCCAAGCTCTCAACTGCGCTTCAAGAGCAAGTCAAGCAGCTCTCTTA 300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 TACTTCCCAACCCCAAGCTCTCAACTGCGCTTCAAGAGCAAGTCAAGCAGCTCTCTG 375

OY 301 GGGGCTGTGATCGGCATTAAGCAGTTCGGCGCTACTTGTGTGTAACCTGCGCTCGGT 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 GGAGGTGTGATCGGCATTAAGCAGTTCGGCGCTACTTGTGTGTAACCTGCGCTCGGT 435

OY 361 GGGGCGCTGGGCGCACCTCCCTTGTGTGTCTACCGCGGACTTGGTAGAGACGAG 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 GGGGCGCTGGGCGCACCTCCCTTGTGTGTCTACCGCGGACTTGGTAGAGACGAG 495

OY 421 TTGGCTCTGATGTGGGCAAGCG--CGCCAGCGTAGTTCCTGCTGTGGGCGACTGT 477
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 CTGGCTCGCCAGCGGCGCAAGGATCTCCAGCGTAGTTCCTGCTGTGGGCGACTGT 555

OY 478 ATCATCAAGATCTTCAAGTGTGATGCGCTGAGGGGCTCTACACAGGTTTCACGCTCT 537
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 CTCACCAAGATCTTCAAGTGTGATGCGCTGAGGGGCTCTACACAGGTTTCACGCTCT 615

OY 538 GTCCAGGCGCATCTTATCTATAGAGCTGCGTACCTCGAGTCTATGANTACGCCAAGGG 597
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 GTCCAGGCGCATCTTATCTATAGAGCTGCGTACCTCGAGTCTATGANTACGCCAAGGG 675

OY 598 ATGCTGCTGACCCCAAGAGAGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 ATGCTGCTGACCCCAAGAGAGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 735

OY 658 ACGGCACTCGAGGGGCTGTCTCTTACCCCTTTGACACTGTTGCTGTAGATGATGATG 717
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 ACAGCCGTGCGGGGCTGTCTCTTATCTATGACACTGTTGCTGTAGATGATGATG 795

OY 718 CAGTCCGCGCGGAAGGGCGGATATTATGACACGGGAGAGTGTGATGATGATGATG 777
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 796 CAGTCCGCGCGGAAGGGCGGATATTATGACACGGGAGAGTGTGATGATGATGATG 855

OY 778 ATTCAAAAGAGCAAGAGAGCCATTTCTTCAAGAGTGCCTGCTCAAAAGTCTGAGA 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 856 ATTCAAAAGAGTGAAGAGAGCCATTTCTTCAAAAGTGTGCTGCTCAAAAGTCTGAGA 915

OY 838 GGCATGGCGGCTGCTTTTGTATTTGTTGTTGATGATGATCAAAAATATGTCTAA 894
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 916 GGCATGGCGGCTGCTTTTGTATTTGTTGTTGATGATGATCAAAAATATGTCTAA 972

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RESULT 5
AAV36480
10 AAV36480 standard; DNA: 1259 BP.

XX AAV36480:
XX

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DT 28-SEP-1998 (first entry)
XX
DE Ant1 cDNA.
XX
KW Ant1; Adenine nucleotide translocator; cloning; screening;
KW DNA Tag dideoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fasciocalcular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease; ss.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 190..1086
FT /tag= a
FT /product= "Ant1 protein"
XX
PN M09819714-A1.
XX
PD 14-MAY-1998.
XX
PF 31-OCT-1997; 97WO-US19882.
XX
PR 01-NOV-1996; 96US-0030017.
XX
RA (UYEM-) UNIV EMORY.
XX
P1 Graham BC, Macgregor GR, Wallace DC;
XX
DR WP1: 1998-286608/25.
XX
PT Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
PS Disclosure; Page 40; 61pp; English.
XX
XX The present sequence is a mouse Ant1 degenerate cDNA sequence, cloned
CC by screening a mouse heart cDNA library with the human Ant1 cDNA as a
CC probe. The Ant1 cDNA sequence was determined by DNA Tag dideoxy
CC terminator cycle sequencing. The Ant1 protein is encoded by the Ant1
CC locus, a nuclear gene on chromosome 8. This protein is required in
CC mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which
CC can then be converted into ATP. An Ant1 homozygous mutant would thus be
CC defective in OXPHOS which results in disease in oxidative metabolism
CC dependent tissues. This mouse Ant1 homozygous mutant can be used as a
CC model system for fasciocalcular humeral muscular dystrophy, hypertrophic
CC cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can
CC be used to test possible therapeutic compounds which increase/mediate ATP
CC and ADP exchange across the mitochondrial membrane independent of Ant1.
XX
XX
SO Sequence 1259 BP; 274 A; 311 C; 339 G; 269 T; 66 other;

```

Query Match 83.5% Score 746.6; DB 19; Length 1259;
Best Local Similarity 90.3% Pred. No. 1e-205;
Matches 810; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

```

OY 1 ATGGGTATCATCGCTTGGAGCTTCTTAAGAGACTTCTGGCGCGGCGCGCTGCC 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 ATGGGGATCAGAGTTTGAGCTTCTTAAGAGACTTCTGGAGGTCGCGCGCGCC 249

OY 61 GTCTCCAAGACCGCGGTCCGCCATCGAGAGGTCAAACTGTCTGTCAGTCCACAT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 GTCTCCAAGACCGCGGTCCGCCATCGAGAGGTCAAACTGTCTGTCAGTCCACAT 309

OY 121 GCCAGCAACAGATCACTGCTGAGAACAGCAGTACAAAGGATCATTTGTTGTGTAGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 GCCAGCAACAGATCACTGCTGAGAACAGCAGTACAAAGGATCATTTGTTGTGTAGA 369

OY 181 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGGTAACTGGCCAACTGATCCGT 240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 370 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGGTAACTGGCCAACTGATCCGT 429

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OY 538 GTCCAGGACATATTATCTATAGAGTCCCTACTTGGAGTGTATGATGACCCAGGG 597
DB 634 GTCCAGGACATCATCTACAGAGCTGCTACTTGGAGTGTATGACACTGCCAAGGG 693
OY 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGACAGTGTG 657
DB 694 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGACAGTGTG 753
OY 658 ACGGACGTGCGAGGCTGCTGTCTTACCCCTTTGACACTGTTCTGTAGATGATG 717
DB 754 ACACGCTGTGCGGCTGTGTCTTATCCGTTTACACTGTTCTGTAGATGATGATG 813
OY 718 CAGTCCGCGCGGAAGGGCGGATATATGACAGGGGACGTTGACTGTGAGAGAG 777
DB 814 CAGTCTGCGCGCAAGGGCGGATATATGACAGGGGACACTTGTGAGAGAG 873
OY 778 ATTCGAAAGACGAGGAGCCGCTTCTTCAAGAGTGTGCTGCAATGCTGTGAGA 837
DB 874 ATTCGAAAGACGAGGAGCCGCTTCTTCAAGAGTGTGCTGCTCAATGCTGTGAGA 933
OY 838 GGCATGGGCGGCTGTTTGTATGTTGTTGATGATGATGATGATGATGATGATG 894
DB 934 GGCATGGGCTGCTGTTTGTATGTTGTTGATGATGATGATGATGATGATGATG 990

RESULT 7
AAD00521 standard: cDNA: 897 BP.

AAD00521:

29-AUG-2000 (first entry)

Human adenine nucleotide translocator ANT3 cDNA.

Human: adenine nucleotide translocator; ANT3; mitochondria; ADP: ATP;
adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
mitochondrial permeability transition; neuroprotective; neurologic;
antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
mitochondrial diabetes and deafness; hyperproliferative disorder;
myoclonic epilepsy red ragged fibre syndrome; ss.

Homo sapiens.

Location/Qualifiers

1..897

/tag= a

/product= "ANT3"

MO200026370-A2.

11-MAY-2000.

03-NOV-1999; 99WO-US25883.

03-NOV-1998; 98US-0185904.

08-SEP-1999; 99US-0334441.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;

Ghosh SS;

WP1: 2000-365619/31.
P-PSDB: AAY71033.
Recombinant construct encoding adenine nucleotide translocator
polypeptide, useful e.g. in screening for potential therapeutic agents

PT against mitochondrial disease -
XX
PS Example 1: Page 166: 175pp: English.
XX
CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is a cDNA
CC encoding adenine nucleotide translocator ANT3 from human brain.
XX
SO Sequence 897 BP: 174 A: 274 C: 287 G: 162 T: 0 other:
Query Match 63.1%: Score 564.2: DB 21: Length 897:
Best Local Similarity 77.6%: Pred. No. 5.5e-153:
Matches 696: Conservative 0: Mismatches 198: Indels 3: Gaps 1:
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DB 1 ATGAGGAGACAGGACATCTCTTCCGCAAGAGCTTCTTGGGAGGACATCTGCCGCGCC 60
OY 61 GTCTCAAGACCGGGTGGCCGCCAGAGAGGCTCAAGCTGCTGTCAGAGTCCACAT 120
DB 61 ATCTCAAGAGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
OY 121 GCCAGCAAGACGATGCTGCTGAGACAGGACAGTCAAGAGGATGATGATGATGATG 180
DB 121 GCCAGCAAGACGATGCTGCGCGGACAGACAGGACAGTCAAGAGGATGATGATGATG 180
OY 181 ATCCCTAAGAGACAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 181 ATCCCAAGAGAGAGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
OY 241 TACTTCCCAAGCAAGCTCTCACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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OY 301 GGGGCTGATGCGGATGAGGACGATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
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DB 361 GGGGCTGATGCGGATGAGGACGATGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
OY 421 TTGGCTGCTGATGCGGAGG--CGGCGCAGGCTGATGCTGCTGCTGCTGCTGCTGCT 477
DB 421 TTGGCTGCTGATGCGGAGG--CGGCGCAGGCTGATGCTGCTGCTGCTGCTGCTGCT 477
OY 478 ATCATCAAGATCTTCAAGTGTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 537
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OY 481 CTGGTGAAGATCAGCAGTGTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 CTGGTGAAGATCAGCAGTGTGAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
OY 538 GTCCAGGACATATTATCTATAGAGTCCCTACTTGGAGTGTATGATGATGATGATGATG 597
DB 541 GTCCAGGACATCATCTACAGAGCTGCTACTTGGAGTGTATGATGATGATGATGATG 600
OY 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTAGAGTGTATGATGATGATGATGATG 657
DB 601 ATGCTGCTGACCCCAAGACGTCACATCTGCTGAGTGTATGATGATGATGATGATG 660
OY 658 ACGGACGTGCGAGGCTGCTGTCTTACCCCTTTGACACTGTTCTGTAGATGATGATG 717

Db	661	ACGGCCGTGGCCGGCGTGGTCTTACCCCTTCGACAGGTTGCGCGCCGCGCATGATATG	720
Oy	718	CAGTCCGCGCGCAAGGGCGCATATATGTACAGGGGACAGTGTGCTGTGAGGAG	777
Db	721	CAGTCCGCGCGCAAGGAGCTGACATCATGTACAGGGGACCGTCTGACTGTTGGAGCAG	760
Oy	778	ATTGCAAAAGACGACGAGCCCAAGCCCTTCTTCAAAAGTGCCTGCTCCATATGCTGAGA	837
Db	781	ATTCTTCAGATGATGAGGGGCGCAAGCCCTTCTTCAAGGCGTGGTGTCCAAAGCTCTCGG	840
Oy	838	GGCATGGCGCGCTCTTTTGTATTTGCTGTATGATGAGATCAAAAATATGCTTAA	894
Db	841	GGCATGGCGCGCGCTCTTCTGCTGTCTGTACGACGAGCTCAAGAGTGATCTAA	897
RESULT 8			
ID	AA505903	standard; cDNA; 897 bp.	
AC	AA505903:		
XX			
Dt	07-SEP-2001	(first entry)	
XX			
De	Human adenine nucleotide translocator-3 (ANT-3) cDNA sequence.		
XX			
KM	Human: adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;		
KM	mitochondrial permeability transition pore component; cell survival;		
KM	mitochondrial core component; mitochondrial related disorder; cancer;		
KM	Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..897	
FT		/*tag= a	
FT		/product= "ANT-3"	
XX			
PN	WO200132876-A2.		
XX			
PD	10-MAY-2001.		
XX			
PF	03-NOV-2000; 2000MO-US30535.		
XX			
PR	03-NOV-1999; 99US-0434354.		
XX			
PA	(MITO-) MITOKOR.		
XX			
P1	Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;		
P1	Velicelcib G, Davis RE;		
XX			
DR	WPI: 2001-291054/30.		
DR	P-PSDB: AAU01200.		
XX			
XX			
PS	New nucleic acid expression constructs, useful for screening for agents		
PT	that alter mitochondrial permeability transition (MPT), comprises		
PT	polynucleotide encoding MPT polypeptide or cyclophilin polypeptide		
PT	fused to energy transfer molecule -		
XX			
XX			
PS	Disclosure; Fig 1; 186pp; English.		
XX			
CC	The present sequence encodes for human adenine nucleotide translocator-3		
CC	(ANT-3) protein. ANT proteins are mitochondrial permeability		
CC	transition (MPT) pore components responsible for mediating transport		
CC	of ADP across the mitochondrial inner membrane. ANT proteins interact		
CC	with other mitochondrial core components e.g. cyclophilins to		
CC	regulate MPT. The present invention relates to a novel nucleic acid		
CC	expression construct comprising a promoter operably linked to a		
CC	polynucleotide encoding a mitochondrial pore component polypeptide		
CC	(e.g. ANT) fused to an energy transfer molecule (ETM) protein		
CC	(e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel		
CC	expression construct can alter mitochondrial membrane permeability		
CC	transition and/or alter the interaction between mitochondrial core		

[illegible]

OS Homo sapiens.
 XX WO200153312-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX 09-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0653450.
 XX 14-SEP-2000; 2000US-0652191.
 XX 19-OCT-2000; 2000US-0693036.
 XX 29-NOV-2000; 2000US-0727344.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 P1 Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 P1 Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 XX WPI: 2001-442253/47.
 DR P-PSDB; AAM39641.
 XX
 XX Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries.
 XX
 XX
 PS Claim 1: SEQ ID NO 1000; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with neurotrophic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC activation/inhibition activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SO Sequence 1212 BP; 247 A; 395 C; 356 G; 214 T; 0 other;

Query Match 62.9%; Score 562.6; DB 22; Length 1212;
 Best Local Similarity 77.5%; Pred. No. 1,8e-152;
 Matches 695; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

OY 1 ATGGGTGATCAGCGCTTGAGCTTCCCTAAAGACTTCCTGCGCGGCGGCTCCCGCTGCC 60
 DB 131 ATGACGGAACAGCGCATCTCTCTCCGCAAGACTCTTGGCCGGAGGCAATCCCGCGCC 190
 OY 61 GTCTCCAGACCGCGGCTCCGCCCATGAGAGGCTCAAACTCTGCTGCGTCCAGCAT 120
 DB 191 ATCTCCAGACGCGCGCTGCTCGCATGAGCGGCTCAACCTCTGCTGAGGTCCAGCAC 250
 OY 121 GCCAGCAACAGATCAGTCTGAGAGCAGTACAAAGGATCATTTGTTGCTGAGA 180
 DB 251 GCCAGCAACAGATCAGTCTGAGAGCAGTACAAAGGATCATTTGTTGCTGAGA 310
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 DB 311 ATCCCTAAGAGAGAGCGCTTCTCTCTGAGAGGCTCAACCTGCGCAAGCTATCCGT 370
 OY 241 TACTTCCCAACCAAGCTCTCAACTTCTGCTTCAAGGACAGTACAAAGGCTCTTCTTA 300
 DB 371 TACTTCCCAACCAAGCTCTCAACTTCTGCTTCAAGGACAGTACAAAGGCTCTTCTTA 430

OY 301 GGGCGGTGCGATAGCGATTCCTGCGCCCTACTTTCGTGTTACCTGCGCCCGGT 360
 DB 431 GGGGCGGTGCAACACACGATTCGTGAGTACTTTCGCGGCAACCTGCGCCCGGT 490
 OY 361 GGGGCGGTGCGCCGACCTCTTTCGTGAGTACTTTCGCGGCAACCTGCGCCCGGT 420
 DB 491 GGTGCGCGCGGCGGACCTCTTTCGTGAGTACTTTCGCGGCAACCTGCGCCCGGT 550
 OY 421 TTGGCTGCTGATGTGGCAGG--CGCGCCGACGCTGAGTTCATGCTGCGGCACTGT 477
 DB 551 CTGGCAGCGGACGTGGAAGATGACAGACAGCGGCGGAGTTCGAGGCGTGGAGATTC 610
 OY 478 ATCATCAAGATTTTCAAGTCTGATGCGCTGAGAGGCGCTTACCAGGTTTCAAGTCTCT 537
 DB 611 CTGGTGAAGATCACAAGTCGACGCGCATCCGCGGCTCTGTACAGGCTTCAAGTCTCTC 670
 OY 538 GTCCAAAGCATATTATCTATGAGCTGCTGAGTCTGAGTCTATGATACCTCCAAAGGG 597
 DB 671 GTGCAAGGATCATATCTATCTACCGGCGGCTTACTTGGGCTATGAGTACGCGCAAGGG 730
 OY 598 ATGCTGCTGACCCCAAGACGTCGACATTTTGTGAGCTGATGATTTCCAGAGTGTG 657
 DB 731 ATGCTGCTGACCCCAAGACGTCGACATTTGTCGAGCTGATGATGCGCGCAAGCGTG 790
 OY 658 ACGGCACTGCGACGGCTGCTCTTACCCCTTTGACACTGTTCTGCTGATGATGATG 717
 DB 791 ACGGCGGTGCGCGGCTGCTCTTACCCCTTTGACACTGTTCTGCTGATGATGATG 850
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 DB 851 CAGTCGCGCGGGAAGGGCGGATTTATGTCACAGGCGACGTTGACTGCGGAGGAG 910
 OY 778 ATTGCAAAAGACGAAGAGCCAGGCTTCTTCAAGAGTCCCTGCTCCATGCTGTGAGA 837
 DB 911 ATCTTCAGAGATGAGAGGGGCGCAAGGCTTCTTCAAGGAGTCCCTGCTCCATGCTGTG 970
 OY 838 GCGATGCGCGGCTTCTTCTTATGCTGTTGATGATGATGATGATGATGATGATGATG 894
 DB 971 GCGATGCGCGGCGGCTTCTTCTTATGCTGTTGATGATGATGATGATGATGATGATG 1027

RESULT 11
 AA160583/c
 ID AA160583 standard; cDNA: 2035 BP.
 AC
 XX AA160583;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 4572.
 XX
 KW Human; neurotrophic; immunosuppressant; cytoskeletal; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia; ss.
 KW
 OS Homo sapiens.
 XX
 XX WO200153312-A1.
 XX
 XX 26-JUL-2001.
 XX
 XX 26-DEC-2000; 2000WO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 XX 25-APR-2000; 2000US-0552317.
 XX 09-JUL-2000; 2000US-0598042.
 XX 19-JUL-2000; 2000US-0620312.
 XX 03-AUG-2000; 2000US-0653450.
 XX 14-SEP-2000; 2000US-0652191.

	PR	19-OCT-2000; 2000US-0693036.
	PR	29-NOV-2000; 2000US-0727344.
	XX	(HYSE-) HYSEO INC.
	XX	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
	P1	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
	P1	Zhao QA, Zhou P, Goodrich R, Drmanac RT;
	XX	WP1: 2001-442253/47.
	DR	P-PsDB: AAM41427.
	XX	
	PT	Novel nucleic acids and polypeptides, useful for treating disorders
	PT	such as central nervous system injuries -
	XX	Claim 1: SEQ ID NO 4572; 10078pp; English.
	CC	The invention relates to human nucleic acids (AA157798-AA161369) and
	CC	the encoded polypeptides (AAM8642-AAM42213) with neurotic,
	CC	immunosuppressant and cytostatic activity. The polynucleotides are useful
	CC	in gene therapy. A composition containing a polypeptide or polynucleotide
	CC	of the invention may be used to treat diseases of the peripheral nervous
	CC	system, such as peripheral nervous injuries, peripheral neuropathy and
	CC	localised neuropathies and central nervous system diseases, such as
	CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
	CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
	CC	utilisation of the activities such as: Immune system suppression,
	CC	activin/inhibin activity, chemotactic/chemokinetic activity, hemostatic
	CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,
	CC	assays for receptor activity, arthritis and inflammation, leukemias and
	CC	C.N.S disorders.
	CC	Note: The sequence data for this patent did not form part of the printed
	CC	specification.
	XX	
S0	Sequence	2035 BP; 398 A; 611 C; 625 G; 401 T; 0 other:
OY	Query Match	62.9%; Score 562.6; DB 22; Length 2035;
	Best Local Similarity	77.5%; Pred. No. 2.3e-152;
	Matches	695; Conservative 0; Mismatches 199; Indels 3; Gaps 14;
Db	1	ATGGGTGATCAGCGTTGGAGCTTCTTAAGACATTCTGCGCGGCGCGTCGCC 60
	1932	ATGACGGAGAACGGGCATCTCTTGCCCAANAACITTTCTTGCCGAGGATGCGCGCCC 1873
OY	61	GTCACGAAGACCAGCGGTGCCCCCATCAGAGAGGATCAAAATGCTCTCAGTCCAGCAT 120
Db	1872	ATCTCCAAAGAGCGCGGTGCTCCGATCGAGGGCGTCAAGTGTCTGCTCAGGTCCAGCAC 1813
OY	121	GCCAGCAACAGATCACTGCTGAGACAAGCATPACAAGGATCATTTGATTGTGTGTGAGA 180
Db	1812	GCCAGCAAGCATGCTGCGCCGACACAAGCATPACAAGGATCATTTGATTGTGTGTGAGA 1753
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Db	1752	ATCCCAAGAGAGAGGCGTCTCTCTCTCTGAGAGGGGCAACTGTCATTTGCGC 1693
OY	241	TACTTCCCAACCACTCTCACTTCACTTCCCTTCAAGAGACAAGTACAAGCAGCTTCTTGA 300
Db	1692	TACTTCCCACTCAAGCGCTCACTTCCCTTCAAGAGATTAAGTACAAACAGATTTCTCTG 1633
OY	301	GGGGGTGTGATTCGGCATTAAGCAGTTCTGSCGCTACTTTCGTGTTAAGCTGAGCTCGCGT 360
Db	1632	GGGGGTGTGATTCGGCATTAAGCAGTTCTGSGAGTACTTTCGTGTTAAGCTGAGCTCGCGC 1573
OY	361	GGGGCGGTGGGGGCACCTCGCTTTCGTTTCTTAACCGGCGAGCATTTGTGTGAAGACAGG 420
Db	1572	GGTGGGGCGGGCGGACCTCTCTCTGCTTCTGTGAACCGGTGATTTGACCAAGACCGGC 1513
OY	421	TTGCGCTGTGATGTGGCAGG---CGCGCCCAAGCGTGAATTCATGTGTGGGACAGTGT 477
Db	1512	CTGGCAGCGGACGTGGGAAGTCAAGGACACAGCGCGAGTTTCCAGAGGCTGTGGACATCTGC 1455
OY	478	ATCATCAAGATTTTCAAGTGTGATGCGCTGAGGGGGGCTTACCAAGGTTTCAACGCTCT 537

Db	1452	CTGGTGAAGATCAACCAAGTCCGACCGGATCCGGGGCTGTACACGAGGCTTCAGTGTCTCC	1393
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Db	1392	GTCCAGGCGCATCATCATCTACCGGGCGGCGCTACTTGGCGGTGTACGATACGGCCAAAGGGC	1333
OY	598	ATGCTGCTCAGACCCCAAGAACGTGCACATTTTGTGACGTGAGATGATTGCCCAAGTGTG	657
Db	1332	ATGCTGCCCGGACCCCAAGAACACACACATCGTGTGTGAGCTGTGATGATTCGCCAGACCGTG	1273
OY	658	ACGGCAGTCCGAGGGCTGCTGTCTTACCCCTTTACACACTGTGTCTGTAGANTATGATG	717
Db	1272	ACGGCCGCTGGCGCGCGCTGTGTCTTACCCCTTTGACACACGGTGGCGGCGCATATGATG	1213
OY	718	CAGTCCGCGCGGAAAGGCGCCGATTTATGTATACACGGGACAGTTGACTGTGGAGAG	777
Db	1212	CAGTCCGCGCGCGGAAAGGAGCGTACATCATGTACACGGGACACGTCGATGTGGAGAG	1153
OY	778	ATTCCAAAGACGAGAGGACCAAGCCCTTCTTCAAGAGTCCCTGCTCAATGTGCTAGA	837
Db	1152	ATTCTTCAAGATGTAGGGGGGCGAAGCCCTTCTTCAAGAGTCCCTGCTCAAGTCTCGCG	1093
OY	838	GGCATTTGGGGGCTGCTTTTGTATTGTGTGTATGATGATCAAAATAATGTCTAA	894
Db	1092	GGCATTTGGGGGCGCTTGTGTGTGTCTGTCTGTACGACGACTCAAGAGGTGATCTAA	1036
RESULT 12			
AD00520	AAD00520 standard; cDNA; 897 BP.		
XX	AAD00520:		
AC	AAD00520:		
AT	29-AUG-2000 (first entry)		
DE	Human adenine nucleotide translocator ANT2 cDNA.		
XX	Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;		
KW	adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;		
KW	mitochondrial permeability transition; neuroprotective; neurotrophic;		
KW	antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;		
KW	antiparkinsonic; cerebrotective; therapeutic; screening; porosis;		
KW	Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;		
KW	diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;		
KW	mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;		
KW	mitochondrial diabetes and deafness; hyperproliferative disorder;		
KW	myoclonic epilepsy red ragged fibre syndrome; ss.		
XX	Homo sapiens.		
OS	Homo sapiens.		
XX	Key		
XX	CDS		
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FT	1..897		
FT	..tag= a		
FT	/product= "ANT2"		
XX	WO200026370-A2.		
XX	11-MAY-2000.		
XX	03-NOV-1999; 99WO-US25883.		
XX	03-NOV-1998; 98US-0185904.		
XX	08-SEP-1999; 99US-0393441.		
PA	(MITO-) MITOKOR.		
XX	Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;		
PI	Shosh SS;		
XX	MPI: 2000-365619/31.		
DR	P-PSDB; AAV71032.		
XX			

CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other:

Query Match 61.9%: Score 553; DB 22; Length 897;
 Best Local Similarity 76.8%: Pred. No. 9.6e-150;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

```

0Y 1 ATGGGTGATCAGCGCTTGAGCTTCTTAAAGCACTTCTGCGCGGCGCGCCGCTGCC 60
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Db 1 ATGACAGATGGCGATTGTCTTGGCCAGAGACTTCTGCGCAGGTGGAGTGGCGAGCC 60
0Y 61 GTCTCCAAAGACCGCGTCCGCCCGCCAGAGGCTCAAACTGCTGCTGCAGCTCCAGCAT 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 ATCTCCAAAGACCGCGTACGCCCGCCAGAGGCTCAAACTGCTGCTGCAGAGCAT 120
0Y 121 CCCAGCAAGACGATCAGCTGCTGAGAACGACATCAAAAGGATCATTTGCTGTGAGTA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 GCCAGCAAGACGATCAGCTGATACCAATCAAAAGGATCATTTAGACTGGTGTGCTGT 180
0Y 181 ATCCCTAAGACGAGCGCTTCTCTCTGAGAGGCTTAACGCGCAACGATATCCGT 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 ATTCCTCAAGAGGAGGAGGAGTCTCTCTCTGAGCGCGGTAACTGCGCAATGTCATGA 240
0Y 241 TACTTCCCGACCCAGCTCTCAACTTGCCTTCAAGAGCAAGTACGACCTCTTTTAA 300
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 TACTTCCCGACCCAGCTCTTAACTTGCCTTCAAGAGTAAATCAAGACGATCTTCTG 300
0Y 301 GGGGCTGTGATCGGCAATAGCACTTGTGGCGCTACTTGTCTGTAACCTGGCGTCCGT 360
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Db 301 GGTGCTGTGAGCAAGAACCACTTGTGGCGCTACTTGTGCAAACTGTGGATCGGCT 360
0Y 361 GGGGCGCTGGGCGCACCTCCCTTGTGCTTACCAGCGCTGAGCTTGGTGAAGACAGG 420
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GGTGCGCGGAGGCGCACATCCCTGTGTTGTGTAACCTCTTGTGATTTTGGCCGTA 420
0Y 421 TTGGCTGCTGATGTGGCA---GGCGCGCCAGCGTATGCTGCTGGCGCATGT 477
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 CTACAGAGTATGTGGTAAAGCTGAGCTGAAGAGAAATTCAGAGCGCTGGTGCATGTC 480
0Y 478 ATCATCAAGATCTTCAAGCTGATGGCTGAGGGGCGCTACCAAGGTTTCAAGCTCTCT 537
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CTGCTTAAGATCTCAAAATCTGATGGGATTTAAGGGCGCTTACCAAGGCTTTAGCTGT 540
0Y 538 GTCCAGGCAATCATTTATATATAGAGCTGCTACTTGGAGAGCTTATGATGATGAGGAG 597
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 GTCCAGGCTATTTATATATCTTACCGAGCGCGCTACTTCCGTATGATGATGAGCAAGG 600
0Y 598 ATGCTGCTGACCCCAAGACGTCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
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Db 601 ATGCTGCTGATCCCAAGACATCACTACATGCTGATGATGATGATGATGATGATGATG 660
0Y 658 ACGGCACTGCGAGGCGCTGCTCTACCCCTTTGACACTGTTTCTGCTGAGTAATGATG 717
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Db 661 ACTGCTGTGGCGGTTGACTTCTATCTTATGACCTTGTGCGCGCGGATGATGATGATG 720
0Y 718 CAGTCCGCGCGAAGGGCGGATTTATGATGACAGGAGAGAGTGTGATGCTGAGAGAG 777
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Db 721 CAGTCCGCGCGAAGGAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 780
0Y 778 ATTGCAAAAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 837
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Db 781 ATTGCTGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
0Y 838 GGCATGGGCGGCTTTTGTATGTGTGTTGATGATGATGATGATGATGATGATGATGAT 894

```

Db 841 GGCATGGGCGGCTTTTGTGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 897

RESULT 14

AA516689 ID AA516689 standard; cDNA: 897 BP.

XX AA516689:

AC 14-FEB-2002 (first entry)

DE DNA encoding human adenine nucleotide translocator 2 (ANT2).

XX Human: adenine nucleotide translocator: ANT: ss;

KW mitochondrial matrix protein.

XX Homo sapiens.

XX Key Location/Qualifiers

FT CDS 1..897

FT /tag= a /product= "Adenine nucleotide translocator 2 (ANT2)."

XX MO200185944-A2.

XX 15-NOV-2001.

PF 11-MAY-2001: 2001WO-US15416.

PR 11-MAY-2000: 2000US-0569327.

XX (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo FR;

P1 Ghosh SS, Moos WH, Pel Y, Carroll AK;

DR WP1: 2002-055598/07.

XX P-PSDB: MAU10379.

PT Novel recombinant expression construct for producing adenine nucleotide

XX translocator polypeptides, comprises a regulated promoter linked to

PS nucleic acid encoding the polypeptide

XX Example 1; Fig 1; 147pp: English.

XX The invention relates to a recombinant expression construct (1)

XX comprising a regulated promoter operably linked to a nucleic acid

XX encoding an adenine nucleotide translocator (ANT) polypeptide, ANT

XX matrix for ADP in the cytosol. (1) is useful for producing recombinant

XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and

XX culturing the host cell. (1) is also useful for targeting a polypeptide

XX expressed as a fusion protein with the polypeptide of interest.

XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is

XX useful for identifying an agent that binds to an ANT polypeptide. ANT

XX ligand is useful for determining the presence of an ANT polypeptide,

XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating

XX ANT from a biological sample, where the ANT ligand is covalently or non-

XX covalently bound to a solid phase. Detectably labeled ANT ligand is also

XX useful for identifying an agent that interacts with an ANT polypeptide.

XX The present sequence represents the coding sequence of human ANT2.

XX Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other:

Query Match 61.9%: Score 553; DB 24; Length 897;

Best Local Similarity 76.8%: Pred. No. 9.6e-150;

Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

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0Y 1 ATGGGTGATCAGCGCTTGAGCTTCTTAAAGCACTTCTGCGCGGCGCGCCGCTGCC 60
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Db 1 ATGACAGATGGCGATTGTCTTGGCCAGAGACTTCTGCGCAGGTGGAGTGGCGAGCC 60

```


Db 353 GGTGCTGTGACAGAGAACCCAGTTTGGCCCTACTTTCAGAGGAATCTGGCATCGGCT 412

OY 361 GGGGGCCGCTGGGGCCACCTCCCTTTCCTTGTCTACCCCTGGACTTTCCTAGACAGG 420

Db 413 GGTGCCGAGGGGCCACATCCCTGTGTTTGTACCCCTTGTGATTTTGGCCGTACCCGT 472

OY 421 TTGGCTGCTGATGTGGCA---GGCGGCCAGCGGTGAGTTCATGTCTGGCGGACTGT 477

Db 473 CTAGCAGCTGATGTGGGTAAAGCTGAGCTGAAGGGAATTCGAGGCCCTCGGTGACTGC 532

OY 478 ATCATCAGATCTTCAAGTGTGATGGCTGAGGGGGCTCTACAGGGTTTCAACGTCTCT 537

Db 533 CTGGTTAAGATCTGACAAATCTGTAGGATTTAAGGCCCTGACCAAGGCTTTAAGCTGTCT 592

OY 538 GTCCAAAGCATCATTTATCTATAGAGCTGCTTACTTGGAGTCTATGATACGCAAGGGG 597

Db 593 GTGCAGGGTATTATCATCTACCGAGCGGCTTCTGCTATCTATGACACTGCMAAGGGA 652

OY 598 ATGCTGCTGACCCCAAGAACGTGCACATTTTGTGAGCTGGATGATGCTCCGAGTGTG 657

Db 653 ATGCTTCCGGATCCCAAGAACACTCAGATCTGATCAGCTGGATGATCCGACAGACTGTC 712

OY 658 ACGGCACTCCAGGGCTGCTGTCTTACCCCTTTGACACTGTTGCTGTAGAAATGATGATG 717

Db 713 ACTGCTGTGGCGGTTGACTTCTCTATCCATTGACACATGTTGGCGCGCATGATGATG 772

OY 718 CAGTCCGCGCGAAGGGCCGATATTATGTCACGGGACAGTTGACTGCTGGAGGAAG 777

Db 773 CAGTCAGGGCGCAAGAACGTGACATCATGTACACAGGCACGCTTGACTGCTGGCGGAAG 832

OY 778 ATTGC-AAAAGAGAGAGAGCCAGGCGCTTCTCAAAAGTGCCCTGCTCCAAAG-TCCTGA 835

Db 833 ATTGCTCCGTGATGAAGAGGCAAGCTTTTTCAGGGGTGATGCTCAATGTCTCA 892

OY 836 GAGGCATGGCGGCTGCTTTTGTATTGTGTGT-ATGATGAGATCAAAAAATATGTCTAA 894

Db 893 GAGGCATGGGTGCTCTTTTGTCTGTCTTGTATGATGAATCAAGAAATACACATAA 952

Search completed: June 22, 2003, 03:22:31
Job time : 196 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 01:58:09 ; Search time 46 Seconds

(without alignments)
5960.196 Million cell updates/sec

Title: US-09-393-441-1

Perfect score: 894
Sequence: 1 atgggtgacacgcttgag.....agatcaaaaatctctaa 894

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 segs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database :
1: /cgn2_6/prodata/1/ina/5A_COMB.seq.*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq.*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/PCBUS_COMB.seq.*
6: /cgn2_6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	746.6	83.5	1259	3 US-08-961-871-11	Sequence 11, Appl
2	745	83.3	1177	3 US-08-961-871-9	Sequence 9, Appl
3	46.6	5.2	1255	1 US-08-518-878B-38	Sequence 38, Appl
4	46.6	5.2	1255	1 US-08-294-522B-38	Sequence 38, Appl
5	46.6	5.2	1255	2 US-08-470-868A-38	Sequence 38, Appl
6	46.6	5.2	1596	2 US-08-807-861A-38	Sequence 38, Appl
7	46.6	5.2	1596	3 US-09-210-681-38	Sequence 38, Appl
8	46.6	5.2	1596	3 US-08-946-719A-38	Sequence 38, Appl
9	42	4.7	1192	4 US-09-142-565-1	Sequence 1, Appl
10	39.2	4.4	810	1 US-08-642-255-60	Sequence 60, Appl
11	37.8	4.2	1643	2 US-08-933-750C-68	Sequence 68, Appl
12	37.8	4.2	1643	3 US-09-234-613-68	Sequence 68, Appl
13	37.4	4.2	997	3 US-09-188-930-23	Sequence 23, Appl
14	37.4	4.2	1816	3 US-09-188-930-262	Sequence 262, App
15	37	4.1	1777	2 US-08-937-466-5	Sequence 5, Appl
16	37	4.1	1777	2 US-09-172-528-5	Sequence 5, Appl
17	37	4.1	1777	3 US-09-318-199-5	Sequence 5, Appl
18	37	4.1	1777	4 US-09-503-579-5	Sequence 5, Appl
19	37	4.1	1949	2 US-08-937-466-3	Sequence 3, Appl
20	37	4.1	1949	2 US-09-172-528-3	Sequence 3, Appl
21	37	4.1	1949	3 US-09-318-199-3	Sequence 3, Appl
22	37	4.1	1949	4 US-09-503-579-3	Sequence 3, Appl
23	37	4.1	2782	2 US-08-937-466-1	Sequence 1, Appl
24	37	4.1	2782	2 US-09-172-528-1	Sequence 1, Appl
25	37	4.1	2782	2 US-09-318-199-1	Sequence 1, Appl
26	37	4.1	2782	4 US-09-503-579-1	Sequence 1, Appl
27	35.4	4.0	216	1 US-07-972-032-46	Sequence 46, Appl

c	28	34.4	3.8	4403765	4	US-09-103-840A-2	Sequence 2, Appl
c	29	34.4	3.8	4411529	4	US-09-103-840A-1	Sequence 1, Appl
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c	31	33.8	3.8	4411529	4	US-09-103-840A-1	Sequence 1, Appl
c	32	33.6	3.8	1594	2	US-08-933-750C-61	Sequence 61, Appl
c	33	33.6	3.8	1594	3	US-09-234-613-61	Sequence 61, Appl
c	34	33.4	3.7	1435	4	US-09-153-804-4	Sequence 4, Appl
c	35	33.4	3.7	68750	3	US-09-335-409-1	Sequence 1, Appl
c	36	33.4	3.7	68750	4	US-09-568-102-1	Sequence 1, Appl
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c	39	33.4	3.7	68750	4	US-09-568-486-1	Sequence 1, Appl
c	40	33.4	3.7	68750	4	US-09-568-472-1	Sequence 1, Appl
c	41	33.4	3.7	68750	4	US-09-443-501A-2	Sequence 1, Appl
c	42	33.4	3.7	71969	4	US-09-567-899-1	Sequence 2, Appl
c	43	33.2	3.7	4843	3	US-08-986-485-1	Sequence 1, Appl
c	44	33	3.7	1386	3	US-08-247-475-16	Sequence 16, Appl
c	45	33	3.7	1386	1	US-08-479-650-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-961-871-11
Sequence 11, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 190..1086
US-08-961-871-11

Query Match 83.5% Score 746.6 DB 3: Length 1259;
 Best Local Similarity 90.3% Pred. No. 5.2e-205;
 Matches 810; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

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Oy 1 ATGGGTGATACAGCTTGAGCTTCTTAAGAGACTTCCTGCGGGGCGGTGCGCCCTCC 60
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Oy 61 GTCCTCAAGACCGCGCTGCGCCCATCGAGAGGGTCAAACTGCTGCTGACAGTCCAGAT 120
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Oy 121 GCCAGCAACAGATCAGTCTGAGAGAGTACAAAGGATCATTTGTTGTGTGAGA 180
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Db 310 GCCAGCAACAGATCAGTCTGAGAGAGTACAAAGGATCATTTGTTGTGTGAGA 369

Oy 181 ATCCCTAGAGAGAGGCTTCTCTCTCTGAGAGGGTAACTGCGCCACAGTATCCGT 240
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Db 370 ATCCCAAGAGAGAGGCTTCTCTCTCTGAGAGGGTAACTGCGCCACAGTATCCGT 429

Oy 241 TACTTCCACCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTTCTTCA 300
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Db 430 TACTTCCACCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTTCTTCA 489

Oy 301 GGGGGTGTGATCGGCATTAAGCAGTCTGCGGCTACTTGTCTGGTAACCTGCGCTCC 360
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Oy 361 GGGGCGCTGCGGCGCCTCTCTCTCTGCTGAGAGGCTGAGTCTGCTGAGAGCAGG 420
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Oy 421 TTGGCTGTGATGTGGCAGGCG--CGCCAGCGTGAGTTTCATGCTGTGGCGCACTGT 477
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Oy 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGGGCTCTACAGAGGTTTCAAC 537
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Db 670 CTCACCAAGATCTTCAAGTCTGATGCGCTGAGAGGGTCTCTACAGAGGTTTCAAG 729

Oy 538 GTCCAAGCATCATTTATATAGAGCTGCTACTTCTGAGAGTCTATGATGAGCAAGGG 597
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Db 730 GTCCAAGCATCATTTATATAGAGCTGCTACTTCTGAGAGTCTATGATGAGCAAGGG 789

Oy 598 ATGCTGCTGACCCCAAGACGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
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Db 790 ATGCTGCTGACCCCAAGACGTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 849

Oy 658 ACGGCACTGCGAGGGGCTGCTCTCAACCCCTTTGACACTGTTTCTGTAAGATGATG 717
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Db 850 ACGGCACTGCGAGGGGCTGCTCTCAACCCCTTTGACACTGTTTCTGTAAGATGATG 909

Oy 718 CAGTCCGCGCGGAAAGGGGCGATATTTATACAGAGGAGCAGTTGACTGCTGAGAG 777
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Db 910 CAGTCCGCGCGGAAAGGGGCGATATTTATACAGAGGAGCAGTTGACTGCTGAGAG 969

Oy 778 ATTGCAAAAGCAAGAGAGCCAGGCTTTTCAAGGCTGCTGCTCAATGTGTGAGA 837
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 970 ATTGCAAAAGCAAGAGAGCCAGGCTTTTCAAGGCTGCTGCTCAATGTGTGAGA 1029

Oy 838 GGCATGGGCGGCTTTTGTATGTGTTGATGATGATGATCAAAAAATATGCTCAA 894
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Db 1030 GGCATGGGCGGCTTTTGTATGTGTTGATGATGATGATCAAAAAATATGCTCAA 1086
  
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RESULT 2

US-08-961-871-9
 : Sequence 9, Application US/08961871

: Patent No. 6013858
 : GENERAL INFORMATION:

: APPLICANT: Wallace, Douglas C.

: APPLICANT: Graham, Brett H.

: APPLICANT: Macgregor, Grant R.

```

: TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
: NUCLEOTIDE TRANSLATOR PROTEIN AND METHODS
: NUMBER OF SEQUENCES: 11
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Greenlee, Minner and Sullivan, P.C.
: STREET: 5370 Manhattan Circle, Suite 201
: CITY: Boulder
: STATE: Colorado
: COUNTRY: US
: ZIP: 80303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/961,871
: FILING DATE: 31-OCT-1997
: CLASSIFICATION: 800
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/030,017
: FILING DATE: 01-NOV-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Ferber, Donna M.
: REGISTRATION NUMBER: 33,878
: REFERENCE/DOCKET NUMBER: 78-96
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (303) 499-8080
: TELEFAX: (303) 499-8089
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1177 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: cDNA to mRNA
: HYPOTHETICAL: NO
: ORIGINAL SOURCE:
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 94..990
: US-08-961-871-9
  
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Query Match 83.3% Score 745; DB 3: Length 1177;
 Best Local Similarity 90.2% Pred. No. 1.4e-204;
 Matches 809; Conservative 0; Mismatches 85; Indels 3; Gaps 1;

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Oy 121 GCCAGCAACAGATCAGTCTGAGAGAGTACAAAGGATCATTTGTTGTGTGAGA 180
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Db 274 ATCCCAAGAGAGAGGCTTCTCTCTCTGAGAGGGTAACTGCGCCACAGTATCCGT 333

Oy 241 TACTTCCACCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTTCTTCA 300
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Db 334 TACTTCCACCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTTCTTCA 393

Oy 301 GGGGGTGTGATCGGCATTAAGCAGTCTGCGGCTACTTGTCTGTAACCTGCGCTCC 360
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Db 394 GGAGCGGTGATCGACATTAAGCAGTCTGCGGCTACTTGTCTGTAACCTGCGCTCTGT 453

Oy 361 GGGGCGCTGCGGCGCCTCTTCTGCTTGTCTACCCGCTGAGACTTTCGTAAGACCAAG 420
  
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db 454 GGGGACGCTGGGGACCTCTGCTGCTACCCCGAGCTTGGTAGGACCAAG 513
421 TTGGCTGCTATGTGGGACGCG---CGCCAGCGTGAATTCATGCTGGGACATG 477
db 514 CTGGCTGGGACGCTGGGACGAGATCTTCCAGGAGAAATTCATGGGCTGGGACATG 573
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db 574 CTCACCAAGATCTTCAAGTCTGAGGCTGAAGGCTCTACAGGGTTTCAAGTCTCT 633
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db 814 CAGTCCGCGCGAAGGGGCGGATATTTATGACAGGGGACAGTTGATGCTGGAGAG 873
cy 778 ATTCGAAAG 837
db 874 ATTCGAAAG 933
cy 838 GCGATGGCGGCTGCTTTTGTATGCTGTTGATGATGATGATGATGATGATGATG 894
db 934 GCGATGGCGGCTGCTTTTGTATGCTGTTGATGATGATGATGATGATGATGATG 990

RESULT 3
US-08-518-878B-38
Sequence 38, Application US/08518878B
Patent No. 5702902
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
US-08-518-878B-38
Query Match 5.2%; Score 46.6; DB 1; Length 1255;
Best Local Similarity 44.2%; Pred. No. 0.00067;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

cy 455 AGTTCATGCTCTGGGACGCTGATCATCAAGATCTTCAAGTGTATGAGGCGG 514
db 143 AGTACCGGGGTGTGTGGGACACATTTCTGACCATGTGCTGATGAGGCGCCCGAAGCC 202
cy 515 TCTACCAAGGTTTCAAGCTCTGTCGCAAGCATCATTTATATAGAGCTGCTACTG 574
db 203 TCTACCAAGGCTGTGTGCGCGCCGCGCAAGATGATGCTTGTGCTGCTGCTGCTG 262
cy 575 GAGTCTATGATGATGCTGCAAGAGGATGCTGCTGACCCCAAGAGCTGACATTTTGTGA 634
db 263 GCCTGTATGATTTCTGTCAACAGATTTCTACCAAGGCGCTGTGAGCATGCGACATGGGA 322
cy 635 GCTGATGATGCTGCGAGAGTGTACGCGAGTGTGCGAGGCTGCTGCTACCCCTTTGACA 694
db 323 GCGGCTCTGACAGGCGACACACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 382
cy 695 CTGTTCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
db 383 ATGTGTAAGGCTCGGATTTCCAAAGCTCAGGCGCGGCTGAGGCTGTGAGATVCAAA 442
cy 755 GCACAGTGTAGCTGTGAGAGAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAG 814
db 443 GCACCGTCAATGCTCTACAGAGACATTTGCGCGAGAGAGAGAGAGAGAGAGAGAG 502
cy 815 GTGCTGTGCTCAATGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 874
db 503 GACCTCTCCCAATGCTGCTGATGATGATGATGATGATGATGATGATGATGATG 562
cy 875 AGATCAAAAATATGTC 891
db 563 ACCTCATCAAGAGATGCC 579

RESULT 4
US-08-294-522B-38
Sequence 38, Application US/08294522B
Patent No. 5741666
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: Compositions and Methods for the
Treatment of Body Weight Disorders, Including Obesity
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/294,522B
FILING DATE: 23-AUG-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-294-522B-38

Query Match 5.2% Score 46.6; DB 1; Length 1255;

Best Local Similarity 44.2% Pred. No. 0.00067;

Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

455 AGTTCATGCTGGGCGACGTATCATCATCTTCAAGTGTGATGCGCTGAGGGGC 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
143 AGTACCGCGGTGTGATGGCCACCATTTCTACCATGTGGCTACTGAGGCCCCCAAGCC 202
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACCAAGGTTTCAACGCTCTCTGTCGAAGGCATCTATATAGAGCTGCGCTACTTGC 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
203 TCTACAAATGGCTGTGGTGGCGGCTGACGCGCAATGAGCTTTGGCTGTGCCGATCG 262
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATACTGCCAAGGGGATGCTCCTGACGCCCAAGAACGTGCACATTTTGTGA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
263 GCGCTATGATTTCTGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCGCACATTTGGGA 322
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GCTGATGATTTGCCAGACTGTGACGGGAGTGGCAGGGGCTGCTGTCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
323 GCGGCTCTCTAGCAGGACACACAGGTGCTGCTGTGCTGTGCGCCAGCCACCG 382
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTGCTGTGAATGATGATGACAGTCCGCGGGAAGGGGCGATATTATATGACACGG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
383 ATGTGTAAGGTCCGATTCGAAGCTCAGGCGCGGCTGAGGTGGTGGAGATACAA 442
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GCACAGTTGACTGCTGAGAGAGATTGCAAAAGACGAGACCAAGCCCTTCTCAAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
443 GCACGCTCAATGCTTCAAGACCATTTGCCGAGAGAGGTTCCGGGCGCTGTGGAAG 502
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
815 GTGCTGTGCAATGTGCTGAGAGCATGGCGGTGCTTTGTATTTGTTGTATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
503 GGACCTTCTCCCATGTGCTGCTAATGCCATTGTCACTGTGCTGAGCTGTGACCTATG 562
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
563 ACCTCATCAAGATGCC 579
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 5

US-08-470-868A-38
Sequence 38, Application US/08470868A
Patent No. 5861485

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis C.
TITLE OF INVENTION: Compositions and Methods for the
TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,868A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-0031-999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66441 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-470-868A-38

Query Match 5.2% Score 46.6; DB 2; Length 1255;

Best Local Similarity 44.2% Pred. No. 0.00067;

Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

455 AGTTCATGCTGGGCGACGTATCATCATCTTCAAGTGTGATGCGCTGAGGGGC 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
143 AGTACCGCGGTGTGATGGCCACCATTTCTACCATGTGGCTACTGAGGCCCCCAAGCC 202
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACCAAGGTTTCAACGCTCTCTGTCGAAGGCATCTATATAGAGCTGCGCTACTTGC 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
203 TCTACAAATGGCTGTGGTGGCGGCTGACGCGCAATGAGCTTTGGCTGTGCCGATCG 262
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATACTGCCAAGGGGATGCTCCTGACGCCCAAGAACGTGCACATTTTGTGA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
263 GCGCTATGATTTCTGTCAAAACAGTTCTACACCAAGGCTCTGAGCATGCGCACATTTGGGA 322
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GCTGATGATTTGCCAGACTGTGACGGGAGTGGCAGGGGCTGCTGTCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
323 GCGGCTCTCTAGCAGGACACACAGGTGCTGCTGTGCTGTGCGCCAGCCACCG 382
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTGCTGTGAATGATGATGACAGTCCGCGGGAAGGGGCGATATTATATGACACGG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
383 ATGTGTAAGGTCCGATTCGAAGCTCAGGCGCGGCTGAGGTGGTGGAGATACAA 442
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GCACAGTTGACTGCTGAGAGAGATTGCAAAAGACGAGACCAAGCCCTTCTCAAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
443 GCACGCTCAATGCTTCAAGACCATTTGCCGAGAGAGGTTCCGGGCGCTGTGGAAG 502
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
815 GTGCTGTGCAATGTGCTGAGAGCATGGCGGTGCTTTGTATTTGTTGTATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
503 GGACCTTCTCCCATGTGCTGCTAATGCCATTGTCACTGTGCTGAGCTGTGACCTATG 562
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
563 ACCTCATCAAGATGCC 579
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111

RESULT 6

US-08-807-861A-38
Sequence 38, Application US/08807861A
Patent No. 5853975

GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/807,861A
FILING DATE: 26-FEB-1997


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CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-807-861A-38

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Query Match      5.2%: Score 46.6; DB 2; Length 1596;
Best Local Similarity 44.2%: Pred. No. 0.00074;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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455 AGTTCATGCTGCTGGGAGCTATCATCAAGATCTTCAAGTGTGATGCGCTGAGGGGC 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
485 AGTACCGCGGTGTATGCGACACATCTGACATGTGCGTGTGAGGGCCCGGAAGCC 544
111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACAGGGCTTTCACAGCTCTGTGTCCAGGCATCATTTATATAGAGCTGCTACTTCG 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111
545 TCTACATGCGGCTGTGCTGCGGCTGCGACCGCCCAATGAGCTTGTGCTGTGCGCATCG 604
111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATGATGCGCAAGGGGATGCTGCTGACCCCAAGACCTGACATTTTGTGA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111
605 GCGTATGATGATGCTGTGTAACAGCTTACACCAAGGGCTCTGACATGCGCATTTGGGA 664
111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GGTGATGATGATGCTGCGACAGTGTGCGAGTGTGCGAGGGCTGCTGCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111
665 GCGCGCTCTGATGACGAGGACGACACAGTGTGCTGCTGTGCTGTGCGCCAGCCAGCG 724
111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTCTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111
725 ATGTGTAAAGGTCGATTCACAGCTCAGGCGCGGCGTGGAGTGTGGATACCAAA 784
111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GGACAGTTGATGCTGTGAGAGGAAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111
785 GCACCGTCAATGCTTACAAAGCAATTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
111 111 111 111 111 111 111 111 111 111 111 111 111 111
815 GTGCGTGTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111
845 GGACCTCTCCCAATGTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 904
111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111
905 ACCTCATCAAGATGCG 921
111 111 111 111 111 111 111 111 111 111 111 111 111 111

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RESULT 7
US-09-210-681-38
Sequence 38, Application US/09210681
Patent No. 6057109
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP

```

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/210,681
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/807,861
FILING DATE: 26-FEB-1997
APPLICATION NUMBER: US 08/518,878
FILING DATE: 23-AUG-1995
APPLICATION NUMBER: US 08/470,868
FILING DATE: 06-JUN-1995
APPLICATION NUMBER: US 08/294,522
FILING DATE: 23-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-066
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 1596 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-210-681-38

```

```

Query Match      5.2%: Score 46.6; DB 3; Length 1596;
Best Local Similarity 44.2%: Pred. No. 0.00074;
Matches 193; Conservative 0; Mismatches 244; Indels 0; Gaps 0;

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455 AGTTCATGCTGCTGGGAGCTATCATCAAGATCTTCAAGTGTGATGCGCTGAGGGGC 514
111 111 111 111 111 111 111 111 111 111 111 111 111 111
485 AGTACCGCGGTGTATGCGACACATCTGACATGTGCGTGTGAGGGCCCGGAAGCC 544
111 111 111 111 111 111 111 111 111 111 111 111 111 111
515 TCTACAGGGCTTTCACAGCTCTGTGTCCAGGCATCATTTATATAGAGCTGCTACTTCG 574
111 111 111 111 111 111 111 111 111 111 111 111 111 111
545 TCTACATGCGGCTGTGCTGCGGCTGCGACCGCCCAATGAGCTTGTGCTGTGCGCATCG 604
111 111 111 111 111 111 111 111 111 111 111 111 111 111
575 GAGCTATGATGATGCTGCGACAGTGTGCGAGTGTGCGAGGGCTGCTGCTACCCCTTTGACA 634
111 111 111 111 111 111 111 111 111 111 111 111 111 111
605 GCGTATGATGATGCTGTGTAACAGCTTACACCAAGGGCTCTGACATGCGCATTTGGGA 664
111 111 111 111 111 111 111 111 111 111 111 111 111 111
635 GGTGATGATGATGCTGCGACAGTGTGCGAGTGTGCGAGGGCTGCTGCTACCCCTTTGACA 694
111 111 111 111 111 111 111 111 111 111 111 111 111 111
665 GCGCGCTCTGATGACGAGGACGACACAGTGTGCTGCTGTGCTGTGCGCCAGCCAGCG 724
111 111 111 111 111 111 111 111 111 111 111 111 111 111
695 CTGTTCTGCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 754
111 111 111 111 111 111 111 111 111 111 111 111 111 111
725 ATGTGTAAAGGTCGATTCACAGCTCAGGCGCGGCGTGGAGTGTGGATACCAAA 784
111 111 111 111 111 111 111 111 111 111 111 111 111 111
755 GGACAGTTGATGCTGTGAGAGGAAGATTTGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 814
111 111 111 111 111 111 111 111 111 111 111 111 111 111
785 GCACCGTCAATGCTTACAAAGCAATTCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 844
111 111 111 111 111 111 111 111 111 111 111 111 111 111
815 GTGCGTGTGATGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 874
111 111 111 111 111 111 111 111 111 111 111 111 111 111
845 GGACCTCTCCCAATGTTGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 904
111 111 111 111 111 111 111 111 111 111 111 111 111 111
875 AGATCAAAAATATATGTC 891
111 111 111 111 111 111 111 111 111 111 111 111 111 111

```


ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
US-08-642-255-60

Query Match 4.4%; Score 39.2; DB 1; Length 810;
Best Local Similarity 50.5%; Pred. No. 0.074;
Matches 95; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

QY 23 TCCTAAGGACTTCCTGGCGGGGGGCGGTGCGCCGCTCCAGACCGCGGTGCCC 82
DB 597 TGCCTCGGACCTCGACGGCCACCGGCTGACCGGCGGACCGCGGTGCGCC 656
QY 83 CCATGAGAGGAGCACTGCTGCTGAGTCCAGATGCCCAAGAGATGAGTTC 142
DB 657 TGGCCCAAGCGGCTCGGCTGATCTAGAGTGACCCAGAGCGGCTGTCATGCCC 716
QY 143 AGAAGCAGTACAAGGATCATTTGTTGTGTGAGATCCCTAAGAGACGAGCTTC 202
DB 717 ACCAGACCGAAGAGAGCTTCACGCTCCGCGAGGTCCGAAACACAGGGGTACCGGCTCCTC 776
QY 203 TCTCTTTC 210
DB 777 TGGCTTTC 784

RESULT 11
US-08-933-750C-68
Sequence 68, Application US/08933750C
Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 1643 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SYNOCAT01
CLONE: 724157
US-08-933-750C-68

Query Match 4.2%; Score 37.8; DB 2; Length 1643;
Best Local Similarity 48.4%; Pred. No. 0.25;
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 151 TACAAGGATCATTTATTTGTGTGTCGAGATTCCTTAAGAGCAGGCGTTCTCTCTTC 210
DB 490 TTCACCTGGCAGCATGATGCTTCGTGAAGATGTGAGCAGCAGGACACAGAGCTTC 549
QY 211 TGGAGGGTAACCTGGCCCAAGCGATCCGTACTTCCCAACCCAGCTCTCACTTCGCC 270
DB 550 TGGAGGCGCTCCCGCCACCTCGTGATGACTGTGCACTACCCGATCTACTTCACCT 609
QY 271 TTCAGAGCAAGTACAAGCAGCTCTTCTTAAGGGGTGTGATCGCATTAAGCAGTTCTGG 330
DB 610 GCCTATGACCAACTGAAGGCTTCCTGTGTGTGTCGAGCCCTGACACTCTGACCTACGCA 669
QY 331 CGCTACTTGTGCTGTAACCTGCGGCTCGGTCGCGGCGG 367
DB 670 CCCATGTGTGCTGCGCGCTGCGCCCTTGGGCGCG 706

RESULT 12
US-09-234-613-68
Sequence 68, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Cortley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive


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CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 75 DENISE DRIVE
CITY: HILLSBOROUGH
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,466
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: 797-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
TELEFAX: (650) 343-4342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-937-466-5

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Query Match 4.1%; Score 37; DB 2; Length 1777;
Best Local Similarity 52.2%; Pred. No. 0.44;
Matches 82; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

OY 728 GGAAGGGGCGGATTTATGTACACGGGACAGTGTGCGAGGAGATTGCCAAG 787
DB 682 GAACGTGAGAGAGAGAGAAATACAGAGGACTATGATGCTTACAGAACATCGCCAGGG 741
OY 788 ACGAAGAGACCAAGGCTTCTTCAAAAGGTGCTGCCATGTCTCTGAGAGGCAATGGCG 847
DB 742 AGGAAGAGAGTCAAGGCGCTGTGGAAGGAGCTTGCGCCACATCACAAGAAATGCCATTG 801
OY 848 GTGCTTTGTATGTGTGTATGATGATGATCAATCAAAA 884
DB 802 TCAACTGTGCTGAGATGCTGACCTACGACATCATCA 838

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Search completed: June 22, 2003, 02:39:02
Job Time : 57 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 02:36:19 : Search time 127 Seconds
(without alignments)
10329.763 Million cell updates/sec

Title: US-09-393-441-1
Perfect score: 894
Sequence: 1 atggtgatcagcttgag.....agatcaaaaataatgctaa 894

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1042519 seqs, 733713590 residues

Total number of hits satisfying chosen parameters: 2085038

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCr_NEM_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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11: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	894	100.0	894	9	US-09-185-904A-1
2	894	100.0	894	10	US-09-811-094-1
3	894	100.0	894	10	US-09-810-644-1
4	873	97.7	1711	9	US-10-198-846-13437
5	757.8	84.8	1196	10	US-09-917-800A-127
6	564.2	63.1	897	9	US-09-185-904A-3
7	564.2	63.1	897	10	US-09-811-094-3
8	564.2	63.1	897	10	US-09-810-644-3
9	562.6	62.9	1212	9	US-10-037-270-687
10	553	61.9	897	9	US-09-185-904A-2
11	553	61.9	897	10	US-09-811-094-2
12	553	61.9	897	10	US-09-810-644-2
13	542.2	60.6	2592	12	US-10-044-090-152
14	488	54.6	1116	9	US-10-171-581-48
15	488	54.6	1116	10	US-09-969-708-213
16	488	54.6	1116	10	US-09-880-107-2096
17	451.2	46.7	2706	9	US-10-103-313-611
18	417.4	45.1	417	9	US-10-198-846-9464
19	402.8	45.1	417	9	US-09-918-995-5864

20	385.8	43.2	484	9	US-09-918-995-6070	Sequence 6070, Ap
21	384.2	43.0	474	9	US-09-918-995-6148	Sequence 6148, Ap
22	368.4	41.2	720	10	US-09-910-943-105	Sequence 105, App
23	325.2	36.4	426	9	US-09-918-995-3021	Sequence 3021, Ap
24	316.8	35.4	415	9	US-09-918-995-3527	Sequence 3527, Ap
25	301.8	33.8	400	9	US-09-918-995-3573	Sequence 3573, Ap
26	290	32.4	501	10	US-09-833-790-161	Sequence 161, App
27	275	30.8	493	9	US-09-918-995-9153	Sequence 9153, Ap
28	272.8	30.5	1156	9	US-10-198-846-6781	Sequence 6781, Ap
29	272.6	30.5	483	9	US-09-918-995-1495	Sequence 1495, Ap
30	272.2	30.5	425	10	US-09-960-352-10722	Sequence 10722, A
31	272.2	30.4	468	9	US-09-918-995-26014	Sequence 26014, A
32	269.2	30.1	513	9	US-09-918-995-37948	Sequence 37948, A
33	242.6	27.1	460	9	US-09-918-995-4700	Sequence 4700, Ap
34	241.6	27.0	464	10	US-09-864-761-1408	Sequence 1408, Ap
35	238.6	26.7	434	10	US-09-960-352-12424	Sequence 12424, A
36	237.2	26.5	410	9	US-09-918-995-16539	Sequence 16539, App
37	236.2	26.4	1125	10	US-09-834-975-995	Sequence 995, App
38	232.6	26.0	283	10	US-09-960-352-14289	Sequence 14289, A
39	231	25.8	485	9	US-09-918-995-8792	Sequence 8792, Ap
40	222	24.8	420	9	US-09-918-995-5524	Sequence 5524, Ap
41	215	24.0	1493	10	US-09-770-445-7	Sequence 7, Appl1
42	214.4	24.0	487	10	US-09-864-761-1488	Sequence 1488, Ap
43	214	23.9	264	10	US-09-960-352-10948	Sequence 10948, A
44	213.2	23.8	957	10	US-09-801-368-251	Sequence 251, App
45	211.6	23.7	1536	10	US-09-734-569-169	Sequence 169, App

ALIGNMENTS

RESULT 1
US-09-185-904A-1
Sequence 1, Application US/09185904A
Patent NO. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSY
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
ORGANISM: Homo sapien
US-09-185-904A-1
Query Match 100.0%; Score 894; DB 9; Length 894;
Best Local Similarity 100.0%; Pred. No. 4.8e-287;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 ATGGGTATATACGCTTGCAGCTTCTTAAGACCTTCTGCGCGCGGCTCGCCCTGCC 60
DB 1 ATGGGTATATACGCTTGCAGCTTCTTAAGACCTTCTGCGCGCGGCTCGCCCTGCC 60
OY 61 GTCTCCAAAGACCGCGCTCGCCCATCGAGAGGCTAAACTGCTGCGAGTCCAGCAT 120
DB 61 GTCTCCAAAGACCGCGCTCGCCCATCGAGAGGCTAAACTGCTGCGAGTCCAGCAT 120
OY 121 GCCAGCAAGACGATCACTGCTGAGAGCACTTACAAAGCATTTGATTCTGCTGAGA 180
DB 121 GCCAGCAAGACGATCACTGCTGAGAGCACTTACAAAGCATTTGATTCTGCTGAGA 180

Oy	18	ATCCGTAAGACAGAGGGCTTCCTCCTCTTGGAGAGGGAAACCTGGCAACGATACCGT	240
Dh	181	ATCCCTTAAGAGCAGAGGCTTCCTCTCTCTCTGAGAGGGTAACCTGGCCAAAGTATCCGT	240
Oy	241	TACTTCCCAACCCAAAGCTCTCAACTTCGCTTCAAGSACAAGTAAAGCAAGCTTCTCTTA	300
Dh	241	TACTTCCCAACCCAAAGCTCTCAACTTCGCTTCAAGSACAAGTAAAGCAAGCTTCTCTTA	300
Oy	301	GGGGGTGTGATTCGGCATTAAGCAGATTCTGGGCTACTTTCGTGTAACCTGGCGTCCGGT	360
Dh	301	GGGGGTGTGATTCGGCATTAAGCAGATTCTGGGCTCACTTTCGTGTAACCTGGCGTCCGGT	360
Oy	361	GGGGCCGCTGGGCCCAACCTCCCTTGGCTTTGGTCTACCCGGCTGACATTGGTAAAGACCAAG	420
Dh	361	GGGGCCGCTGGGCCCAACCTCCCTTGGCTTTGGTCTACCCGGCTGACATTGGTAAAGACCAAG	420
Oy	421	TTGGCTGTGATGTGGGCAAGCGCGGCCAGCGTGAATTCCATGCTGTGGGCACATGTATC	480
Dh	421	TTGGCTGTGATGTGGGCAAGCGCGGCCAGCGTGAATTCCATGCTGTGGGCACATGTATC	480
Oy	481	ATCAAGATCTTCAAGTCTGATGGCGTGAAGGGGCGCTACAGAGGGTTTCAACGTCTGTGC	540
Dh	481	ATCAAGATCTTCAAGTCTGATGGCGTGAAGGGGCGCTACAGAGGGTTTCAACGTCTGTGC	540
Oy	541	CAAGGCATCTTATCTATAGAGCTGCCTACTTTCGAGTCTATGATTACTGCCAAGGGATG	600
Dh	541	CAAGGCATCTTATCTATAGAGCTGCCTACTTTCGAGTCTATGATTACTGCCAAGGGATG	600
Oy	601	CTGCGTCAGCCCAAGAAAGCTGCACATTTTGTGACCTGGATGATTTGCCCAAGGTGACG	660
Dh	601	CTGCGTCAGCCCAAGAAAGCTGCACATTTTGTGACCTGGATGATTTGCCCAAGGTGACG	660
Oy	661	GCAGTGGCAGGGCTGCTCTTACCCGCTTGAACACTTGTGCTGAGTAAATGATGATGACG	720
Dh	661	GCAGTGGCAGGGCTGCTCTTACCCGCTTGAACACTTGTGCTGAGTAAATGATGATGACG	720
Oy	721	TCCGGCGCGAAAGGGGCCCATATTATATGACACGGGGAAGTTGACTGCTGGAGGAATTT	780
Dh	721	TCCGGCGCGAAAGGGGCCCATATTATATGACACGGGGAAGTTGACTGCTGGAGGAATTT	780
Oy	781	GCAAAAGACAGACGACCAAGGCTTCTTCAAAAGTGGCTGGTCCAAATGTCTAGAAGGC	840
Dh	781	GCAAAAGACAGACGACCAAGGCTTCTTCAAAAGTGGCTGGTCCAAATGTCTAGAAGGC	840
Oy	841	ATGGCGCGTCTTTTATTTGGTGTGTTATGATGATCAAAAATATGTCTAA	894
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: RESULT 2
: US-09-811-094-1
: Sequence 1, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Ellen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pol, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (AMT)
: FILE OF INVENTION: NOVEL AMT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D4
: CURRENT APPLICATION NUMBER: US/09/811,094
: CURRENT FILING DATE: 2001-03-14
: NUMBER OF SEQ. ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 894
: TYPE: DNA
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: ORGANISM: Homo sapien
US-09-811-094-1

Query Match      100.0%; Score 894; DB 10; Length 894;
Best Local Similarity 100.0%; Pred. NO. 4 Be-287;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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[illegible]

RESULT 3
US-09-810-644-1
; Sequence 1, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:

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: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Cleveland, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yashong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D3
: CURRENT APPLICATION NUMBER: US/09/810,644
: NUMBER OF FILING DATE: 2001-03-14
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 1
: LENGTH: 894
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-810-644-1

Query Match      100.0%; Score 894; DB 10; Length 894;
Best Local Similarity 100.0%; Pred. No. 4.8e-287;
Matches 894; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGGGTGATCAGCCTTGGAGCTTCTTAAGAGACTTCTGCGCGCGGTGCGCGCTGCC 60
Oy 61 GTCTCCAAAGACCGCGTCCGCCCATGAGAGGGTCAAACTGCTGTCGACAGTCCAGCAT 120
Db 61 GTCTCCAAAGACCGCGTCCGCCCATGAGAGGGTCAAACTGCTGTCGACAGTCCAGCAT 120
Oy 121 GCCAGCAACAGATCAGTCTGAGAGAGTACAAAGGATCATGATGTTGTTGAGAG 180
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Oy 241 TACTTCCCAACCCAGCCTCTCAACTTCCGCTTCAAGAGAGTCAAGAGAGTCTTCTTA 300
Db 241 TACTTCCCAACCCAGCCTCTCAACTTCCGCTTCAAGAGAGTCAAGAGAGTCTTCTTA 300
Oy 301 GGGGGTGGATGGGATGAAGAGCTTGGCGCTACTTTGCTGTAACCGTGGCGTCCGGT 360
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Db 361 GGGGGCTGGGGCCACCTCCCTTCTTGTCTTACCCGCTGGAGCTTGGCTAGACACAG 420
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Oy 541 CAAGGATCATTTATATAGAGCTGCTACTTGGAGTATATATGCTGCAAGGGGATG 600
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Oy 601 CTGCTGACCCCAAGAGCTGCAATTTTGTGAGCTGATGATGAGTCCAGAGTGTGACG 660
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Oy 781 GCAAAAGACGAGAGAGCGCAAGGCTTCTCAAAAGGCGCGGCAATGCTGAGAGGCG 840
Db 781 GCAAAAGACGAGAGAGCGCAAGGCTTCTCAAAAGGCGCGGCAATGCTGAGAGGCG 840
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RESULT 4
US-10-198-846-13437
: Sequence 13437, Application US/10198846
: Publication No. US2003009974A1
: GENERAL INFORMATION:
: APPLICANT: Lillie, James
: APPLICANT: Xu, Yongyao
: APPLICANT: Wang, Youzhen
: APPLICANT: Steilmann, Kathleen
: TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
: TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
: FILE REFERENCE: MRI-049
: CURRENT APPLICATION NUMBER: US/10/198,846
: CURRENT FILING DATE: 2002-07-18
: PRIOR APPLICATION NUMBER: 60/306,220
: NUMBER OF SEQ ID NOS: 14084
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 13437
: LENGTH: 1711
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
: LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
: LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
: LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
: OTHER INFORMATION: n = A,T,C or G
: FEATURE:
: NAME/KEY: misc.feature
: LOCATION: 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
: LOCATION: 1445, 1446, 1447, 1448, 1449, 1710, 1711
: OTHER INFORMATION: n = A,T,C or G
: US-10-198-846-13437

Query Match      97.7%; Score 873; DB 9; Length 1711;
Best Local Similarity 99.1%; Pred. No. 6.4e-280;
Matches 889; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

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Db 181 ATCCCTAAGAGAGAGCGCTTCTCTCTCTGAGAGGGTAACTGGCCCAAGTGAATCCGT 240
Oy 347 ATCCCTAAGAGAGAGCGCTTCTCTCTCTGAGAGGGTAACTGGCCCAAGTGAATCCGT 406
Db 347 ATCCCTAAGAGAGAGCGCTTCTCTCTCTGAGAGGGTAACTGGCCCAAGTGAATCCGT 406
Oy 241 TACTTCCCAACCCAGCCTCTCAACTTGGCGCTTCAAGAGAGTCAAGAGAGTCTTCTTA 300
Db 241 TACTTCCCAACCCAGCCTCTCAACTTGGCGCTTCAAGAGAGTCAAGAGAGTCTTCTTA 300

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407 TACTTCCCAACCAAGCTCTCACTCGCTTCAAGACAAGTACAAAGACAGCTCTCTTA 466
Cy 301 GGGGGTGTGATTCGGCATTAAGACATTTCTGGGGCTACTTTGCTGTAACTGCGCTCCGGT 360
Db 467 GGGGTGTGATTCGGCATTAAGACATTTCTGGGGCTACTTTGCTGTAACTGCGCTCCGGT 526
Cy 361 GGGGGCTGTGGGGCAGCTCTGCTTTGCTTTGCTACCGGGGAGCTTTGGTACGACGAGG 420
Db 527 GGGGGCTGTGGGGCAGCTCTGCTTTGCTTTGCTACCGGGGAGCTTTGGTACGACGAGG 586
Cy 421 TTGGCTGCTGATGTGGGCAAGCG---CGCCCAAGCTGATTCATGCTGTGGGAGCTGT 477
Db 587 TTGGCTGCTGATGTGGGCAAGCGGGCGCCAGCTGATTCATGCTGTGGGAGCTGT 646
Cy 478 ATCATCAAGATCTTCAAGCTGTGATGCTTGAAGGGGCTTACAGGGCTTTCACGCTCT 537
Db 647 ATCATCAAGATCTTCAAGCTGTGATGCTTGAAGGGGCTTACAGGGCTTTCACGCTCT 706
Cy 538 GTCCAGGATCATTTATCTATAGAGCTGCTTGGAGCTTATGATGCTGCTGCTGCTGCT 597
Db 707 GTCCAGGATCATTTATCTATAGAGCTGCTTGGAGCTTATGATGCTGCTGCTGCTGCT 766
Cy 598 ATGCTGCTGACCCCAAGAACGTCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657
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Cy 658 AGCGCAGTCCGAGGCTGCTTCTTACCCTTTTGACACTGTTCTGCTGATGATGATG 717
Db 827 AGCGCAGTCCGAGGCTGCTTCTTACCCTTTTGACACTGTTCTGCTGATGATGATG 886
Cy 718 CAGTCCGGCGGGAAGGGCGGATATATGACAGGGGAGAGTGAAGCTGCTGAGAGAG 777
Db 887 CAGTCCGGCGGGAAGGGCGGATATATGACAGGGGAGAGTGAAGCTGCTGAGAGAG 946
Cy 778 ATTGCAAAAGACGAAGAGAGCCAGGCTTTCTTCAAAAGTGCCTGCTCAATGTGCTGAG 837
Db 947 ATTGCAAAAGACGAAGAGAGCCAGGCTTTCTTCAAAAGTGCCTGCTCAATGTGCTGAG 1006
Cy 838 GGCATGGCGGCTGCTTTTGTATTTGTGTTGATGATGATGATCAAAAATATGTCTAA 894
Db 1007 GGCATGGCGGCTGCTTTTGTATTTGTGTTGATGATGATGATCAAAAATATGTCTAA 1063

RESULT 5
US-09-917-800A-1327
Sequence 1327, Application US/09917800A
Patent No. US20020119462A1
GENERAL INFORMATION:
APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5038-US
CURRENT APPLICATION NUMBER: US/09/917, 800A
CURRENT FILING DATE: 2001-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,880
PRIOR FILING DATE: 2000-11-02
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/290,645
PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: US 60/292,336
PRIOR FILING DATE: 2001-05-22
PRIOR APPLICATION NUMBER: US 60/295,798
PRIOR FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: US 60/297,457
PRIOR FILING DATE: 2001-06-13
PRIOR APPLICATION NUMBER: US 60/298,884

PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: US 60/303,459
PRIOR FILING DATE: 2001-07-09
NUMBER OF SEQ ID NOS: 1740
SOFTWARE: Patentl Ver. 2.1
SEQ ID NO 1327
LENGTH: 1196
TYPE: DNA
ORGANISM: Rattus norvegicus
OTHER INFORMATION: Genbank Accession No. US20020119462A1 D12770
US-09-917-800A-1327

Query Match 84.8%; Score 757.8; DB 10; Length 1196;
Best Local Similarly 91.1%; Pred. No. 1.2e-241;
Matches 817; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

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Cy 61 GTCTCCAAAGACCGCGGCTGCGCCCATGAGAGGGTCAAACTGCTGTGACAGTGCACAT 120
Db 136 GTCTCCAAAGACCGCGGCTGCGCCCATGAGAGGGTCAAACTGCTGTGACAGTGCACAT 195
Cy 121 GCCAGCAAGACAGATCACTGCTGAGAACAGTACAAAGGATCATTTGATGTGTGAGAG 180
Db 196 GCCAGCAAGACAGATCACTGCTGAGAACAGTACAAAGGATCATTTGATGTGTGAGAG 255
Cy 181 ATCCCTAAGAGAGAGGCTTCTCTCTTCTGAGAGGGTAACTGCGGCAAGCTGATCCGT 240
Db 256 ATCCCTAAGAGAGAGGCTTCTCTCTTCTGAGAGGGTAACTGCGGCAAGCTGATCCGT 315
Cy 241 TACTTCCCAACCCAGAGCTTCAACTTCCCTTCAAGAGAGTCAAGAGTCAAGAGCTTCTTA 300
Db 316 TACTTCCCAACCCAGAGCTTCAACTTCCCTTCAAGAGAGTCAAGAGTCAAGAGTCTTCT 375
Cy 301 GGGGCTGTGATGCGCATTAAGCAAGTCTGCGCTACTTCTGCTGAACCTGCGCTCGGT 360
Db 376 GGAAGTGTGATGCTGCTTAAGCAAGTCTGCGCTACTTCTGCTGAACCTGCGCTCGGT 435
Cy 361 GGGGCGGCTGGGGCAACCTCCCTTTGCTTGTACCGGCTGAGCTTGTGTAGAGCAGG 420
Db 436 GGGGCACTGCGGCTTACCTCTCTCTGCTGTCTTACCACTGAGCTTGTGTAGAGCAGG 495
Cy 421 TTGGCTGCTGATGTGGGCAAGCG---CGCCCAAGCTGATTCATGCTGTGGGAGCTGT 477
Db 496 CTGGCTGCGAGCTGGGCAAGGAGATCTTCCACGCTGATTCATGCTGTGGGAGCTGT 555
Cy 478 ATCATCAAGATCTTCAAGCTGTGATGCTTGAAGGGGCTTACAGGGTTCACGCTCT 537
Db 556 CTCACCAAGATCTTCAAGCTGTGATGCTTGAAGGGGCTTACAGGGTTCACGCTCT 615
Cy 538 GTCCAGGATCATTTATCTATAGAGCTGCTTGGAGCTTATGATGCTGCTGAGAGGG 597
Db 616 GTCCAGGATCATTTATCTATAGAGCTGCTTGGAGCTTATGATGCTGCTGAGAGGG 675
Cy 598 ATGCTGCTGACCCCAAGAACGTCACATTTTGTGAGCTGATGATGCTGCGCAGAGTGT 657
Db 676 ATGCTGCTGACCCCAAGAACGTCACATTTTGTGAGCTGATGATGCTGCGCAGAGTGT 735
Cy 658 AGCGCAGTCCGAGGCTGCTTCTTACCCTTTGACACTGCTGCTGCTGCTGCTGCTGCT 717
Db 736 ACAGCGCTGGCGGGCTGTGCTTCTTACATTTTGAACACTGCTGCTGCTGCTGCTGCT 795
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Db 796 CAGTCCGGCGGGAAGGGCGGATATATGATGATGATGATGATGATGATGATGATGATG 855
Cy 778 ATTGCAAAAGACGAAGAGAGCCAGGCTTCTTCAAAAGTGCCTGCTGCTCAATGTGCTGAG 837
Db 856 ATTGCAAAAGATGAAGAGAGCCAGGCTTCTTCAAAAGTGCCTGCTGCTCAATGTGCTGAG 915

Qy 838 GGCATGGCGCTTTTGTATGTTGATGATGATCAAAAATATGCTTAA 894
 Db 916 GGCATGGCGGCTTTTGTATGTTGATGATGATGATCAAAAATATGCTTAA 972

RESULT 6
 US-09-185-904A-3

Sequence 3, Application US/09185904A
 Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Cleveneger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185,904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 897

TYPE: DNA

ORGANISM: Homo sapien

US-09-185-904A-3

Query Match 63.1%; Score 564.2; DB 9; Length 897;
 Best Local Similarity 77.6%; Pred. No. 2.9e-177;

Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Qy 1 ATGGGATGATCAGCGCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCTGCGCGCTGCG 60
 Db 1 ATGAGGAGACAGCGCTTCTTCTTCTGCGCGCGGAGACTTCTGCGCGCGGCTGCGCGCG 60
 Qy 61 GTCTCCAGACCGCGGCTGCG 120
 Db 61 ATCTCCAGACCGCGGCTGCG 120
 Qy 121 GCCAGAACATGATGCTGATGAGAGGATCAAGAGGATCATGATGATGATGATGATGATA 180
 Db 121 GCCAGAACATGATGCTGATGAGAGGATCAAGAGGATCATGATGATGATGATGATGATA 180
 Qy 181 ATCCCTAAGAGAGAGGCTTCT 240
 Db 181 ATCCCTAAGAGAGAGGCTTCT 240
 Qy 241 TACTTCCCACTCAAGCTTCAACTTCCCTTCAAGAGGATCAAGAGGATCAAGAGGATCAAG 300
 Db 241 TACTTCCCACTCAAGCTTCAACTTCCCTTCAAGAGGATCAAGAGGATCAAGAGGATCAAG 300
 Qy 301 GGGGGTGGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Db 301 GGGGGTGGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
 Qy 361 GGGGGTGGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Db 361 GGGGGTGGATGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
 Qy 421 TGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 Db 421 TGGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 477
 Qy 478 ATCATCAAGATCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 Db 478 ATCATCAAGATCTTCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 537
 Qy 538 GTCCAGGATCATTTATAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 597
 Db 538 GTCCAGGATCATTTATAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 597

Db 541 GTGAGGAGCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 600
 Qy 598 ATGCGCGGACCGCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 657
 Db 601 ATGCGCGGACCGCCAGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
 Qy 658 ACGGAGTGCAGAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 717
 Db 661 ACGGAGTGCAGAGGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 720
 Qy 718 CAGTCCGCGGAGAGGCGCGCATATTTATGATGATGATGATGATGATGATGATGATGATG 777
 Db 721 CAGTCCGCGGAGAGGCGCGCATATTTATGATGATGATGATGATGATGATGATGATGATG 780
 Qy 778 ATTCGAAAAG 837
 Db 781 ATTCGAAAAG 840
 Qy 838 GGCATGGCGGCTTTTGTATGTTGATGATGATGATCAAAAATATGCTTAA 894
 Db 841 GGCATGGCGGCTTTTGTATGTTGATGATGATGATCAAAAATATGCTTAA 897

RESULT 7
 US-09-811-094-3

Sequence 3, Application US/09811094
 Patent No. US2001004414A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Cleveneger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Miller, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR

FILE REFERENCE: 660088.420D4

CURRENT APPLICATION NUMBER: US/09/811,094

CURRENT FILING DATE: 2001-03-14

NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 3

LENGTH: 897

TYPE: DNA

ORGANISM: Homo sapien

US-09-811-094-3

Query Match 63.1%; Score 564.2; DB 10; Length 897;
 Best Local Similarity 77.6%; Pred. No. 2.9e-177;

Matches 696; Conservative 0; Mismatches 198; Indels 3; Gaps 1;

Qy 1 ATGGGATGATCAGCGCTTGGAGCTTCTTAAGGACTTCTGCGCGCGGCTGCGCGCTGCG 60
 Db 1 ATGAGGAGACAGCGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 60
 Qy 61 GTCTCCAGACCGCGGCTGCG 120
 Db 61 ATCTCCAGACCGCGGCTGCG 120
 Qy 121 GCCAGAACATGATGCTGATGAGAGGATCAAGAGGATCATGATGATGATGATGATGATGATA 180
 Db 121 GCCAGAACATGATGCTGATGAGAGGATCAAGAGGATCATGATGATGATGATGATGATGATA 180
 Qy 181 ATCCCTAAGAGAGAGGCTTCT 240
 Db 181 ATCCCTAAGAGAGAGGCTTCT 240
 Qy 241 TACTTCCCACTCAAGCTTCAACTTCCCTTCAAGAGGATCAAGAGGATCAAGAGGATCAAG 300
 Db 241 TACTTCCCACTCAAGCTTCAACTTCCCTTCAAGAGGATCAAGAGGATCAAGAGGATCAAG 300

APPLICANT: Wehrman, Tom
 APPLICANT: Xue, Aidong J.
 APPLICANT: Yang, Yonghong
 APPLICANT: Wang, Jian-Rui
 APPLICANT: Zhou, Ping
 APPLICANT: Ma, Yundong
 APPLICANT: Wang, Dunrui
 APPLICANT: Wang, Zhiwei
 APPLICANT: Tillinghast, John
 APPLICANT: Drmanac, Radoje T.
 TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
 TITLE OF INVENTION: Polypeptides
 FILE REFERENCE: 78ACIP2B
 CURRENT APPLICATION NUMBER: US/10/037,270
 CURRENT FILING DATE: 2002-01-04
 PRIOR APPLICATION NUMBER: 09/552,317
 PRIOR FILING DATE: 2000-04-25
 PRIOR APPLICATION NUMBER: 09/488,725
 PRIOR FILING DATE: 2000-01-21
 NUMBER OF SEQ ID NOS: 1104
 SOFTWARE: PC_FIL_genes Version 1.0
 SEQ ID NO: 687
 LENGTH: 1212
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (131)..(1027)
 US-10-037-270-687

Query Match 62.9% Score 562.6; DB 9; Length 1212;

Best Local Similarity 77.5%; Pred. No. 1.1e-173; Matches 695; Conservative 0; Mismatches 199; Indels 3; Gaps 1;

1 ATGGGTGATCAGCGTGGAGCTTCTTAAGAGACTTCGCGCGGCGGCGCGCTCC 60
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 131 ATGAGGAAAGAGGCGATCTCTCGCCAAAGACTTCTGGCGGAGGATCGCCCGCC 190
 61 GTCTCCAGAGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 191 ATCTCCAGAGCG 250
 121 GCCAGCAAGAGATGCTGAGAGAGTACAAAGGATCATGATTTGTGTGTGA 180
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 251 GCCAGCAAGAGATGCTGAGAGAGTACAAAGGATCATGATTTGTGTGTGA 310
 181 ATCCCTAAGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 311 ATCCCAAGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 370
 241 TACTTCCCAAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 371 TACTTCCCAAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 430
 301 GGGGTGTGAGGATGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTG 360
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 431 GGGGTGTGAGGATGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTG 490
 361 GGGGTGTGAGGATGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTGAGAGAGTCTG 420
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 491 GGTGGGCGGCG 550
 421 TTGGCTGTGATGTGGGCGAG---CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 477
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 551 CTGGAGCGGAGCTGTGGAGAGTCAAGAGAGCGGAGTTCGAGGCGCTGGAGAGTGC 610
 478 ATCATCAGAGATTTAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGTGT 537
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 611 CTGGTGAAGATCAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGTGT 670
 538 GTCAAGAGATCATTTATAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 597
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 671 GTGAGAGGATCATTTATAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 730

598 ATGCGCTGACCCCAAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAG 657
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 731 ATGCTCCCGAGACCCCAAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 790
 658 ACGGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 717
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 791 ACGGCGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 850
 718 CAGTCCGCGCGGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAG 777
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 851 CAGTCCGCGCGGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAG 910
 778 ATGCAAGAGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 837
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 911 ATCTTCAAGATGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAG 970
 838 GCGATGCGCGGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 894
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 971 GCGATGCGCGGAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAGAGAGTGTAG 1027

RESULT 10

US-09-185-904A-2

Sequence 2, Application US/09185904A

Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.

APPLICANT: Davis, Robert E.

APPLICANT: Clevenger, William

APPLICANT: Miller, Sandra Eileen

APPLICANT: Miller, Scott W.

APPLICANT: Szabo, Tomas R.

APPLICANT: Ghosh, Soumitra S.

TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE

TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASS

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 660088.420

CURRENT APPLICATION NUMBER: US/09/185,904A

CURRENT FILING DATE: 1998-11-03

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO: 2

LENGTH: 897

TYPE: DNA

ORGANISM: Homo sapien

US-09-185-904A-2

Query Match 61.9% Score 553; DB 9; Length 897;
 Best Local Similarity 76.8%; Pred. No. 1.6e-173; *
 Matches 689; Conservative 0; Mismatches 205; Indels 3; Gaps 1;

1 ATGGGTGATCAGCGTGGAGCTTCTTAAGAGACTTCGCGCGGCGGCGCGCTCC 60
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 1 ATGAGAGAGCGGAGTGTCTCTCGCCAAAGACTTCTGGAGAGTGTGGCGCGCGAGC 60
 61 GTCTCCAGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 121 ATCTCCAGAGCGGCGGAGTGTCTGAGAGAGTGTCTGAGAGAGTGTCTGAGAGAGT 120
 121 GCCAGCAAGAGATGCTGAGAGAGTGTCTGAGAGAGTGTCTGAGAGAGTGTCTGAG 180
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 181 ATCCCTAAGAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 241 ATCCCAAGAGAGCGGAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 241 TACTTCCCAAGAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
 301 GGGGTGTGAGATGAGAGAGTGTCTGAGAGAGTGTCTGAGAGAGTGTCTGAGAGAGT 360

```

Db      301  GGTGGTGTGACAAACAGAACACCAGCTTTTGGCCCTACTTTGGACGGGAAATCTGGCATCGGCT 360
Oy      361  GGGGCGCGTGGGGCCACCTCCCTTTGCTTTGTCTAACCCGCTGACTTTGCTAGGACCAG 420
Db      361  GGTGCGGACGGGCGCCACACATCCCTGTGTTTGTGTACCCCTTGATTTTCCCGTACCCT 420
Oy      421  TTGGCTGCTGATGTTGGGCA---GGCGGGCCGACGCTGAGTTCCATGCTCTGGCGGACTG 477
Db      421  CTAGACGCTGATGTGGTGAAACCTGAGCTGACGAAGGAAATTCGAGGCGCTCGGTGACTGC 480
Oy      478  ATCATCAAGATCTTCAACTCTGATGCGCTGAGAGGGGCTCTACACAGGCTTCAACGCTCT 537
Db      481  CTGGTTAGATCTACAAATCTGATGTCGATTAAGGGCGCTGTACCAAGCGTTTAAACGTGCT 540
Oy      538  GTCCAAAGCATCATTTATCTATAGAGCTGCTTACTTTCGAGTCTATGATATCTGCCAAGGG 597
Db      541  GTGCGAGGCTATTATCATCTATACCGACCGCGCTACTTCGATATGACACTGCAAAAGGGA 600
Oy      598  ATGCGCTGACCCCAAGACAGCTGACATTTTGTGAGTGGTGATTTCCCGAGACTGTG 657
Db      601  ATGCTCTCCGCACTCCCAAGAACACTACATCGTCAATCAGCTGATGTCACAGACTGTTC 660
Oy      658  ACGCAGTGTGCGAGGGCTCTGTCTACCCCTTTGACACTGTTGCTGCTGTAATGATGATG 717
Db      661  ACTGCTGTGGCGGGGTGACTTCTCATCCATTTGACACCGCTTGCCCGCGCATGATGATG 720
Oy      718  CAGTCCGCGCCGGAAGGGGCGCATTTTATGTACAGGGGACAGTGCATGCTGAGAGAG 777
Db      721  CAGTCAGGGCCCAAGGAACGTACATCATGTACACAGGACGACTTGACGTGGCGGGAAG 780
Oy      778  ATTGCAAAAGACGAGAGGACCCAAAGCCCTTCTTCAAAAGCGCTGCTCAATGCTGAGAGA 837
Db      781  ATTGCTGCTGATGAAGGAGGAGCAACTTTTTTCAAGGGTGATGGTCCATATGTTCTCAGA 840
Oy      838  GCGATGGCGGCTGCTTTTGTATTTGTTGTATGTATGATGAGATCAAAAATATGTCTAA 894
Db      841  GGCATGCGTGGCTGTTTGTGCTTCTTGTATGATGAATCAAGAACTACACATTA 897

RESULT 11
US-09-811-094-2
: Sequence 2, Application US/09811094
: Patent No. US20010044144A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Miller, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pei, Yezhong
: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
: FILE REFERENCE: 660088.420D4
: CURRENT APPLICATION NUMBER: US/09/811,094
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 897
: TYPE: DNA
: ORGANISM: Homo sapien
US-09-811-094-2

```

Query Match	61.9%	Score 553	DB 10	Length 897
Best Local Similarity	76.8%	Pred. No. 1.6e-173		
Matches	689	Conservative	0	Mismatches 205; Indels 3; Gaps 1

07	1	ATGGGTATCACCGCTTGGACGCTTCTCTAAAGACGCTTCCTGGCCGGGCGGCTCCCGCTGCC	60

Db	1	ATGACAGATGCCCGCATTTGCTTGGCCAAAGACCTTCGTGGAGAGTGGAGTGGCCGCGAGCC	60
Oy	61	GTCTCCAAAGACCCGGGTGCGCCCGCCATTCAGAGGGTCAAACTGCTGTGCAAGTCCAGCAT	120
Db	61	ATCTCCAAAGAGGGGGGTAGCGGCCATTCAGCGGGGTCAAGCTCTCTGTGAGGTGAGCAT	120
Oy	121	GCCAGCAAAACAGATAGTGTGTGAGAGAGTCAAGAGGATCATATTGATTGTGGTGGAC	180
Db	121	GCCAGCAAAACAGATCTACTGTCAAGATTAAGCAATTAACAAAGCATTTATAGACTGCGTGGCT	180
Oy	181	ATCCCTAAGGAGACAGGGCTTCCTCTCCTTTCTGGAGGGGTAACTGTGGCCAAAGTATCCGT	240
Db	181	ATTCGCAAGAGACAGAGATTCTGTCTTCCTTGGCGGGTAACCTGGCCAAATGTCAACAGA	240
Oy	241	TACTTCCCGCCACCAAGCTCTCACTTGGCTTCAAGAGACAAGTCAACAGCACTTCTTTA	300
Db	241	TACTTCCCGCCACCAAGCTTAACTTCGCTTCAAGATTAATATACAAAGACAGATCTTCGTG	300
Oy	301	GGGGGTGTGATTCGGCATTAAGCAGTTCGTGGCGCTACTTTCGTGTAACTGTGGCGTCCGT	360
Db	301	GGTGTGTGTGACAAAGAGAACCCAGTTTGTGGCGCTACTTTCGACGGGAATCTGGCATGGGT	360
Oy	361	GGGGCGCGTGGGGCCACCTCCCTTTGCTTTGTCTAACCGCTGACACTTCTTAGACACAG	420
Db	361	GGTGGCGGAGGGGGCCACATCCCTGTGTTTGTGTACCCCTTGATTTTTCGCGTACCCCT	420
Oy	421	TTGGCTGTGTAGTGTGGGCA---GGCGCGCCGACGCTGATTCATATGCTGTGGGCAACTG	477
Db	421	CTAGAGCTGTAGTGTGGGTAAAGCTGTAGCTGAAGAGGAATTTTCAGAGCGCTCGGTGACTGC	480
Oy	478	ATCATCAAGATCTTCAAGCTGTATGAGCGCTGAGAGGGGCTTACACAGGTTTCAACGCTCT	537
Db	481	CTGGTTAAGATCTCAAAATCTGATGGATTAAAGGCGCTGTACCAAGCGTTTAAAGCTCT	540
Oy	538	GTCCAAAGCATATTATCTATAGAGACTGCTTACTTTCGGAGTCTTATGATACTGCCAAGGG	597
Db	541	GTGACAGGTATTATCATCTATACCGACCGCCCTTACTTCGTATCTATGACACTCCAAAGGGA	600
Oy	598	ATGCTGCTGACCCCAAGACGTGCACATTTTGTGACGTGATGATTTCCAGAGATGTG	657
Db	601	ATGCTTCGCGATCCCAAGACACTACATCGTCACTACGTGATGATGCCACAGACTGTG	660
Oy	658	ACGGCAGTGCAGAGGCGTCTGTCTTAACCCCTTTCGACACTGTTCGTAGTAATGATGATG	717
Db	661	ACTGCTGTGCGCGGGTACTTCTCATTTGACATTTTTCACCGCTCGCGCGCATGTATGATG	720
Oy	718	CAGTCCGGCGGAAAAGGGCGGATTTATGTACAGGGGACAGTTGATGATGCTGAGAGAA	777
Db	721	CAGTGAAGGGCGCAAAAGACACTGACATCTTGTACACAGGACACCTGTGACTGTGCGGGA	780
Oy	778	ATTGCAAAAGACGAAGAGCAAGGCCCTTCTTCAAAAGTGCCTGTGCTCAATGTGCTGAGA	837
Db	781	ATTGCTCTGTATGAAGGAGCAAAAGCTTTTTCAGGGGTCATGTGCTCAATGTTCACAGA	840
Oy	838	GGCATATGGCGGCTTTTCTGTATGTGTGTATGTATGTATGTATGATCAAAATAATATCTC	894
Db	841	GGCATATGGGTGGCTTTTGTCTGTCTGTCTGTGTATGTATGTATGAATCAAAAGTACACAT	897

RESULT 12
US-09-810-644-2
: Sequence 2, Application US/09810644
: Patent No. US20020012992A1
: GENERAL INFORMATION:
: APPLICANT: Anderson, Christen M.
: APPLICANT: Davis, Robert E.
: APPLICANT: Clevenger, William
: APPLICANT: Wiley, Sandra Eileen
: APPLICANT: Willer, Scott W.
: APPLICANT: Szabo, Tomas R.
: APPLICANT: Ghosh, Soumitra S.
: APPLICANT: Moos, Walter H.
: APPLICANT: Pel, Yachong

: TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
: TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
: FILE REFERENCE: 660088.420D3
: CURRENT APPLICATION NUMBER: US/09/810.644
: NUMBER OF SEQ ID NOS: 37
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 897
: TYPE: DNA
: ORGANISM: Homo sapien
: US-09-810-644-2

Query Match 61.9% Score 553: DB 10: Length 897:
Best Local Similarity 76.8% Pred. No. 1.6e-173:
Matches 689: Conservative 0: Mismatches 205: Indels 3: Gaps 1:

Cy 1 ATGGGTATACAGCTTGGAGCTTCTTAAGAGCTTCCGCGCGGCGCGCGCTGCC 60
Db 1 ATGAGAGATGGCGGATTCCTCTGCGCAAGAGACTTCCTGGCAGAGTGGAGTGGCGCGCAGCC 60
Cy 61 GTCTCCAGAGCGCGGCTGCGCCCATCGAGAGGTCAACTGCTGCTGCGAGTCCAGCAT 120
Db 61 ATCTCCAGAGCGCGGCTGCGCCCATCGAGAGGTCAACTGCTGCTGCGAGTCCAGCAT 120
Cy 121 GCCAGCAACAGATCAGTGTGAGAGAGTACAAAGGAGTCAATGATGTTGTGTGAGA 180
Db 121 GCCAGCAACAGATCAGTGTGAGAGAGTACAAAGGAGTCAATGATGTTGTGTGAGA 180
Cy 181 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGCTTAACCTGCGCCAGCGTATCCCT 240
Db 181 ATCCCTAAGAGAGCGGCTTCTCTCTCTGAGAGGCTTAACCTGCGCCAGCGTATCCCT 240
Cy 241 TACTTCCCGCCAGAGCTCTCAACTTCCCTTCAAGAGAGTCAAGAGAGCTCTTCTTA 300
Db 241 TACTTCCCGCCAGAGCTCTCAACTTCCCTTCAAGAGAGTCAAGAGAGCTCTTCTG 300
Cy 301 GGGGGTGTGAGTGGCATTAAGAGTTCGGGCTCTTGTGCTGATTAACCTGCGCGCTG 360
Db 301 GGGGGTGTGAG 360
Cy 361 GGGGGTGTGAG 420
Db 361 GGGGGTGTGAG 420
Cy 421 TTGGCTGTGATGTGGCA---GGCGCGCCAGCGTCAATGCTGTGGCGCATCT 477
Db 421 TTGGCTGTGATGTGGCA---GGCGCGCCAGCGTCAATGCTGTGGCGCATCT 477
Cy 478 ATCATCAAGATCTTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Db 478 ATCATCAAGATCTTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Cy 538 GTCCAGGATCATATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
Db 538 GTCCAGGATCATATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 597
Cy 597 GTCCAGGATCATATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
Db 597 GTCCAGGATCATATATATATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 657
Cy 657 ATGCTGCTGAG 717
Db 657 ATGCTGCTGAG 717
Cy 717 ACTGCTGTGGCGGATGAGTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
Db 717 ACTGCTGTGGCGGATGAGTCTTCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 777
Cy 777 ATGCTGCTGAG 837
Db 777 ATGCTGCTGAG 837

Cy 838 GGCATGGCGGCTGCTTGTATGTGCTGTATGATGATGATGATGATGATGATGATGAT 894
Db 841 GGCATGGCGGCTGCTTGTATGTGCTGTATGATGATGATGATGATGATGATGATGAT 897

RESULT 13
US-10-044-090-152
Sequence 152: Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVA
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044.090
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 152
LENGTH: 2592
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc-feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11
NAME/KEY: unsure
LOCATION: 1131, 1929
OTHER INFORMATION: a, t, c, g, or other
US-10-044-090-152

Query Match 60.6% Score 542.2: DB 12: Length 2592:
Best Local Similarity 77.4% Pred. No. 1e-169:
Matches 696: Conservative 0: Mismatches 198: Indels 5: Gaps 3:

Cy 1 ATGGGTATACAGCTTGGAGCTTCTTAAGAGCTTCTGCGCGG-GGCGGCTGCCGTGC 59
Db 207 ATGAGAGATGGCGGATTCCTCTGCGCAAGAGACTTCTGGCGGAGATGCGCGCGC 266
Cy 60 GGTGCAAGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 118
Db 267 CATCTCCAGAGAGCGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 326
Cy 119 ATCCAGCAACAGATCAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 178
Db 327 ACCGAG 386
Cy 179 GATTCCTTAAG 238
Db 387 GATTCCTTAAG 446
Cy 239 GTTACTTCCCGCCAGAGCTCTCAACTTCCGCTTCAAGAGAGAGAGAGAGAGAGAG 298
Db 447 GCTACTTCCCGCCAGAGCTCTCAACTTCCGCTTCAAGAGAGAGAGAGAGAGAGAG 506
Cy 299 TAGGGGTGTGAG 358
Db 507 TGGGGGGGTGTGAG 566
Cy 359 GTGGGGCGGTGTGAG 418
Db 567 GCGGGGCGGTGTGAG 626
Cy 419 GGTGGGTGTGAG 475
Db 627 GCGGGGCGGTGTGAG 686
Cy 476 GTATCATCAAGATCTTCAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
Db 687 GCGGTGTGAG 746
Cy 536 CTGTCCAGAGAGATCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
Db 747 CCGTCCAGAGAGATCATTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 806

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 22, 2003, 03:07:09 ; Search time 1081 seconds
(Without alignments)
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Title: US-09-393-441-1
Perfect score: 894
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 809774376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estlinu:*
5: em_estlov:*
6: em_estlpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estlom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrc:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761.4	85.2	964	12	BG673955 602620126
2	739.6	82.7	859	9	AL556492 AL556492
3	733.2	82.0	1073	13	BM230491 BM230491
4	717.4	80.2	925	13	B1754652 B1754652
5	715.8	80.1	909	9	AL561542 AL561542
6	712.4	79.7	1043	13	BM466452 BM466452

7	709.6	79.4	990	13	B1545249
8	697.2	78.0	1033	13	B1408731
9	681.2	76.2	879	13	B1458358
10	676.6	75.7	882	13	BM459526
11	670.4	75.0	907	13	B1667026
12	665.8	74.5	862	14	B0214399
13	664.2	74.3	888	13	B1412906
14	663	74.2	946	13	B1256359
15	659.4	73.8	946	14	B0947818
16	654.6	73.2	869	12	BG666092
17	652	72.9	887	13	B1755550
18	649.6	72.7	826	13	B1666964
19	643.8	72.0	1058	13	B1410853
20	637.6	71.3	789	14	B0572174
21	633.8	70.9	868	13	B1525539
22	633	70.8	800	13	B1546581
23	632.4	70.7	929	14	B0963574
24	629.8	70.4	863	13	B1408467
25	628.2	70.3	826	13	B1410725
26	627.8	70.2	828	13	B1544547
27	627.4	70.2	882	14	B0435016
28	624.2	69.8	785	13	B1088005
29	622.8	69.7	828	13	B1411055
30	615.8	68.9	905	13	B1598151
31	609.4	68.2	947	13	B1416038
32	608.4	68.1	849	13	B1414676
33	607.6	68.0	757	13	B1092477
34	607.2	67.9	1004	14	B0964708
35	606.2	67.8	826	13	B1904612
36	604.4	67.6	921	14	B0938203
37	604.4	67.6	928	9	AL578737
38	601.4	67.3	741	13	B1669668
39	600.2	67.1	887	13	B1732570
40	599.6	67.1	824	12	BE780630
41	597	66.8	721	14	B0548008
42	596	66.7	816	12	BG707401
43	593.6	66.4	1040	12	BF794987
44	592.8	66.3	911	13	B1735372
45	592.2	66.2	907	13	B1603210

ALIGNMENTS

RESULT 1
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LOCUS 602620126F1 NCI_GCAP_Skn3 Homo sapiens CDNA clone IMAGE:4745430 5',
DEFINITION BG673955 mRNA sequence.
ACCESSION BG673955
VERSION BG673955.1 GI:13905347
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 964)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://image.llnl.gov
Plate: LLM10592 row: d column: 07
High quality sequence stop: 835.
Location/Qualifiers
1..964

FEATURES
Source

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/organism="Homo sapiens"
/job_xref="taxon:9606"
/clone="IMAGE:4745430"
/clone_1lb="NCI-CGAP-Skn3"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: skin; Vector: pCNAV-SPOK6; Site_1: Nci1; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI-CGAP library."
BASE COUNT      188 a      249 c      310 g      217 t
ORIGIN

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Query March	85.2%	Score 761.4	DB 12	Length 964	
Best Local Similarity	95.2%	Pred. No. 3.7e-102			
Matches 829	Conservative	0	Mismatches 36	Indels 6	Gaps 4

Oy	1	ATGGGTGATCAACGCTTGGAGCGCTTCTTAAGGACCTCTCGGCGGGGCGGTGCGCGCTGC	60
Dh	92	ATGGGTGATCAACGCTTGGAGCGCTTCTTAAGGACCTCTCGGCGGGGCGGTGCGCGCTGC	151
Oy	61	GTCCTCAAGACCGCGGTGCGCCCATCGAGAGGGTCAAACTGCTCTCGAGCTCCAGCAT	120
Dh	152	GTCCTCAAGACCGCGGTGCGCCCATCGAGAGGGTCAAACTGCTCTCGAGCTCCAGCAT	211
Oy	121	GCCAGCAACAGATAGTGTGTGAGAGCAAGTCAAAAGGATCATTTGTTGTGTGACA	180
Dh	212	GCCAGCAACAGATAGTGTGTGAGAGCAAGTCAAAAGGATCATTTGTTGTGTGAGA	271
Oy	181	ATCCCTTAAGAGACAGGGCTTCCTCTCTTGTGAGGGGTAACTGCGCAAGCTGATCCGT	240
Dh	272	ATCCCTTAAGAGACAGGGCTTCCTCTCTCTTGTGAGGGGTAACTGCGCAAGCTGATCCGT	331
Oy	241	TACTTCCCCACCCCAAGCTCTCAACTTCGCTTCAAGGACAACTAGACAAGAGCTCTTCTTA	300
Dh	332	TACTTCCCCACCCCAAGCTCTCAACTTCGCTTCAAGGACAACTAGACAAGAGCTCTTCTTA	391
Oy	301	GGGGGTGTGATCGGCATPAGCAGTTCTTGCGCTACTTTGCTGTGTAACCTGGCGTCGCT	360
Dh	392	GGGGGTGTGATCGGCATPAGCAGTTCTTGCGCTACTTTGCTGTGTAACCTGGCGTCGCT	451
Oy	361	GGGGCGGTGGGGGCCACGCTTGTGTGCTACTACCGCTGACCTTGTGTGAGACCAAG	420
Dh	452	GGGGCGGTGGGGGCCACGCTTGTGTGCTACTACCGCTGACCTTGTGTGAGACCAAG	511
Oy	421	TTGGCTGCTGATGTGGGCGAGGCG--CCGCCAGCTGAGATTGCATGTGTGGGCGACTGT	477
Dh	512	TTGGCTGCTGATGTGGGCGAGGCGCGCCGCCAGCTGAGATTGCATGTGTGGGCGACTGT	571
Oy	478	ATCATCAAGATCTTCAAGTCTGTGATGSGCTGAGGGGGCTCTACAGAGGTTTCAACGCTCT	537
Dh	572	ATCATCAAGATCTTCAAGTCTGTGATGSGCTGAGGGGGCTCTACCA--GGTTTCAACGCTCT	630
Oy	538	GTCCAAGGCATCTTATCTATPAGAGCTGCTACTTCGAGTCTATGATPACTGCCCAAGGG	597
Dh	631	GTCCAAGGCATCTTATCTATPAGAGCTGCTACTTCGAGTCTATGATPACTGCCCAAGGG	690
Oy	598	ATGCGCGCTGACCCCAAG--AACGTGACACTTTTGTGAGCTGGATGATGGCCAGAGTGT	656
Dh	691	ATGCGCGCTGACCCCAAGAGAGCTGACACTTTTCTGTGAGCTGGATGATGGCCAGAGTGT	750
Oy	657	GACGGCAGTGGCAGGGCTGTGTCTTACCCCTTTGACACTGTTGCTGTGTAATGATGAT	716
Dh	751	GACGGCAGTGGCAGGGCTGTGTCTTACCCCTTTGACACTGTTGCTGTGTAATGATGAT	810
Oy	717	GCAGTCCCGCGGAAAGGGCGCATATTATGTACACGGGGACAGTTGACTGCTGGAGGAA	776
Dh	811	GCAGTCCCGCGGAAAGGGCGCATATTATGTACACGGGGACAGTTGACTGCTGGAGGAG	870
Oy	777	GATTGCAAAAGACGAAGAGCCAAAGCCCTTCTTCAAAAGGTGCTGTGCCAATGTGCTGAG	836
Dh	871	AATTG--GAAGACGAAGGACCCAAAGGCTTCTTTCAAGGTGCTTGTCCATGTTGCTGGA	929
Oy	837	AGGCATGGCGGCTTTTGTATTGCTGTTG 867	

Db	930	GAGGCATGGCAGGCGCTTTAGCATGGCGTGATG	960
RESULT 2			
LOCUS	AL556492		
DEFINITION	AL556492 L11_NFL006.PL2 Homo sapiens cDNA clone CS00K006YA17 5	859 bp	mrna linear EST 16-FEB-2001
ACCESSION	AL556492		
VERSION	AL556492.1	GI:12899215	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 859)		
TITLE	Li, W.B., Gruber, C., Jesse, J. and Polayes, D.		
JOURNAL	Full-length cDNA libraries and normalization		
COMMENT	Unpublished (2001)		
CONTACT	Contact: Genoscope		
Genoscope - Centre National de Sequencage			
BP 191 91006 Evry cedex - France			
Email: segrete@genoscope.cns.fr , Web : www.genoscope.cns.fr .			
FEATURES	Location/Qualifiers		
source	1..859		

	BASE COUNT	ORIGIN
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Query Match	82.7%: Score 739.6; DB 9; Length 859;	
Best Local Similarity	98.8%: Pred. No. 4.5e-196;	
Matches 765:	Conservative 1; Mismatches 5; Indels 3; Gaps 2;	
OY	1 ATGGGTATCACGCTTGAGAGCTTCTCTAAAGACTTTCCTGGCGGGCGGCTGCCGCTGCC	60
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OY	61 GTCTTCAAGACCGCGGTGCGCCGCCATCGAGAGGGGTCAAACTGCTGTGACAGTCCAGCAT	120
Db	147 GTCTTCAAGACCGCGGTGCGCCGCCATCGAGAGGGGTCAAACTGCTGTGACAGTCCAGCAT	206
OY	121 GCCAGCAAAACAGATCAGTGTCTGACAGACAGTACAAAGGATCATTTGTTGTGTGAGA	180
Db	207 GCCAGCAAAACAGATCAGTGTCTGACAGACAGTACAAAGGATCATTTGTTGTGTGAGA	266
OY	181 ATCCCTTAAGAGACAGGGGCTTCTCTCCCTTCTGAGAGGGGTAACTGGGCAACGTATCCGT	240
Db	267 ATCCCTTAAGAGACAGGGGCTTCTCTCCCTTCTGAGAGGGGTAACTGGGCAACGTATCCGT	326
OY	241 TACTTCCCAACCAAGCTTCTCACTTCCGCTTCAAGAGACAATGACAGACGCTTCTTGA	300
Db	327 TACTTCCCAACCAAGCTTCTCACTTCCGCTTCAAGAGACAATGACAGACGCTTCTTGA	386
OY	301 GGGGGGTGGAGTGGCGCAATACCACTTTCGGGGGTACATTGCTGTAACTGGGCGCTCCGGT	360
Db	387 GGGGGGTGGAGTGGCGCAATACCACTTTCGGGGGTACATTGCTGTAACTGGGCGCTCCGGT	446
OY	361 GGGGCGGCTGGGGCGACCTCCCTTGTCTTACCCGCGTGACATTTGGTAGAGCAGG	420

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Db 447 GGGGGCGCTGGGGCCACTCCCTTGTGTTGTCTACCCGCTGACCTTGGTACGACG 506
Oy 421 TTGGCTGCTGATGAGGCA--GGCGGCCCAAGCGTGAATGCTGCTGGGCGACTGA 478
Db 507 TTGGCTGCTGATGAGGCAAGGCGGCCGAGCGTGAATGCTGCTGGGCGACTGA 566
Oy 479 TCATCAGATCTTCAAGCTGATGAGGCGGCTCTACGAGGTTTCAAGCTCTG 538
Db 567 TCATCAGATCTTCAAGCTGATGAGGCGGCTCTACGAGGTTTCAAGCTCTG 626
Oy 539 TCAGAGCATATATCTATAGAGTGGCTCTGAGTGTGATGATGATGATGATGATG 598
Db 627 TCAGAGCATATATCTATAGAGTGGCTCTGAGTGTGATGATGATGATGATG 686
Oy 599 TGCTGCTGAGCCCAAGACGTCACATTTTGTGAGCTGATGATGATGATGATG 658
Db 687 TGCTGCTGAGCCCAAGACGTCACATTTTGTGAGCTGATGATGATGATGATG 746
Oy 659 CGGAGTGGCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 718
Db 747 CGGAGTGGCAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 806
Oy 719 AGTCCGCGCGGAAAGGCGCGATATATGATGATGATGATGATGATGATGATG 772
Db 807 AGT-CGGCGGAAAGGCGCGATATATGATGATGATGATGATGATGATGATG 859

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RESULT 3
LOCUS BM230491/3 1073 bp mRNA linear EST 31-JAN-2002
DEFINITION K0296810-3 NIA Mouse unfertilized egg cDNA library (long) Mus
ACCESSION BM230491
VERSION Mus230491.1 GI:17793731
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.

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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Steag, C.A.,
Martin, P., Aliba, K., Tanaka, T. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Unfertilized Egg cDNA Library
(Long)
Unpublished (2001)
JOURNAL Laboratory of Genetics
COMMENT Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: K0296 row: B column: 10
Seq primer: -21M13 Forward
High quality sequence stop: 1073
POLYA-Yes.

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FEATURES Source

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Location/Qualifiers
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/organism="Mus musculus"
/strain="C57BL/6J"
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/clone_11b="NIA Mouse Unfertilized Egg cDNA Library (Long)"
/tissue_type="Unfertilized Egg"
/lab_host="DH10B"
/Note="Vector: pSPORT1 (Invitrogen); Site_1: SalI; Site_2:
NotI; Mouse cDNA project by the Laboratory of Genetics,
National Institute on Aging (NIA), Intramural Research
Program, NIH (http://igsun.grc.nia.nih.gov/cDNA). This is
a long-transcript enriched cDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
extracted from a pool of 1488 unfertilized eggs.

```

Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen: 5'-pGACTAGTCTAGATCGGAGCGGCCCGCTTTTCTTTT-3'], treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer SalI-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.5 kb. The library was constructed by Yulan Piao (NIA).

BASE COUNT 249 a 309 c 272 g 237 t 6 others
ORIGIN

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Query Match 82.0%; Score 733.2; DB 13; Length 1073;
Best Local Similarity 89.9%; Pred. No. 3.1e-194;
Matches 807; Conservative 0; Mismatches 87; Indels 4; Gaps 2;
1 ATGGGTGATCAAGGCTTGGAGCTTCTTAAGAGCTTCCGGCGGCGCGGCGCTCC 60
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Db 899 GTCTNCCAGACCGCGGTGCGCCCATGAGAGGCTCAAACTGCTGTCAGATCCACA 840
Oy 120 TGCCAGCAACAGATCACTGCTGAGAGAGCTACAAAGGATCATTTGTTGCTGAG 179
Db 839 TGCCAGCAACAGATCACTGCTGAGAGAGCTACAAAGGATCATTTGTTGCTGAG 780
Oy 180 AATCCCTAAGAGAGAGGCTTCTCTCTCTTGTGAGAGGCTAACTGCGCAAGTATCCG 239
Db 779 AATCCNCCAGAGAGAGGCTTCTCTCTCTTGTGAGAGGCTAACTGCGCAAGTATCCG 720
Oy 240 TTACTTCCCAAGAGAGCTTCAACTTCTGCTTGAAGAGAGAGAGAGAGAGAGAGCTTCT 299
Db 719 GTACTTCCCAAGAGAGCTTCAACTTCTGCTTGAAGAGAGAGAGAGAGAGAGAGCTTCT 660
Oy 300 AGGGGTGATGAGGCTTAAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 359
Db 659 GGAAGGCTGATGAGGCTTAAGAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 600
Oy 360 TGGGCGCGTGGGCGCACTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 419
Db 599 TGGGCGCGTGGGCGCACTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 540
Oy 420 GTTGGCTGCTGATGAGGCGAGGCG---CGCCAGAGCTGAGTTCATGCTGAGGCGACTG 476
Db 539 GCTGGCTGCGAGGCGAGGCGAGGAGTCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 480
Oy 477 TATATCAAGATCTTCAAGTGTGATGAGGCTGAGGAGGCTTACAGAGGCTTCAAGCTCTC 536
Db 479 TCTCACCAAGATCTTCAAGTGTGAGGAGGCTTCAAGGAGGCTTCAAGCTCTC 420
Oy 537 TGTCAGAGGATCTTATCTATAGAGTGGCTTGTGAGGAGTCTATGATGATGATGATGATG 596
Db 419 TGTCAGAGGATCTTATCTATAGAGTGGCTTGTGAGGAGTCTATGATGATGATGATGATG 360
Oy 597 GATGCTGCTGAGCCCAAGAGAGCTGATTTTGTGAGCTGATGATGATGATGATGATG 656
Db 359 GATGCTGCTGAGCCCAAGAGAGTGTGATGATGATGATGATGATGATGATGATGATGATG 300
Oy 657 GAGCGAGTGGCAGAGGCTGCTCTTACCCCTTGTGAGCTGCTGCTGATGATGATGATG 716
Db 299 GAGCGAGTGGCAGAGGCTGCTCTTACCCCTTGTGAGCTGCTGCTGATGATGATGATG 240
Oy 717 GCACTGCGGCGGAAAGGCGGATATATGATGATGATGATGATGATGATGATGATGATG 776

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Dh 239 GCAGTGTGGCCGGAAGGGGCTGATATATGTACAGGGGACATTGACTGTGAGGAA 180
Oy 777 GATTGCAAAAGACGAGAGAGCCAGAGCCTTTCTCAAGAGTGGCTGCTCAATGCTGAG 836
Dh 179 GATTGCAAAAGATGAGAGAGCCAGAGCCTTTCTCAAGAGTGGCTGCTCAATGCTGAG 120
Oy 837 AGGCATGGCGGCGCTTTTGTATTGGTGTGTATGATGATCAAAAATATGCTGTA 894
Dh 119 AGGCATGGCGTGGCTTTTGTATTGGTGTGTATGATGATCAAAAATATGCTGTA 62

RESULT 4

LOCUS B1754652 925 bp mRNA linear EST 25-SEP-2001
DEFINITION 603025339F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5196080 5',
B1754652
ACCESSION B1754652
VERSION B1754652.1 GI:15746230
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NIH-MGC http://mgc.ncl.nih.gov/

REFERENCE 1 (bases 1 to 925)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@rs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLAM11490 row: m column: 09
High quality sequence stop: 791.

FEATURES

source

Location/Qualifiers

1..925

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5196080"

/clone_1ib="NIH_MGC_114"

/lab_host="DH10B"

/note="Organ: brain; Vector: PCMV-SPORT6; Site: 1; Not1;
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male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb. Insert size
range 1-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 019. Note:
this is a NIH-MGC Library."

BASE COUNT 184 a 249 c 294 g 198 t

ORIGIN

Query Match 80.2%; Score 717.4; DB 13; Length 925;
Best Local Similarity 96.5%; Pred. No. 7.7e-190;
Matches 798; Conservative 0; Mismatches 21; Indels 8; Gaps 6;

Oy 1 ATGGGTGATCAGCGCTTGAGAGCTTCTTAAGAGACTTCTGCGCGGCGGCTGCGCTGCC 60
Dh 98 ATGGGTGATCAGCGCTTGAGAGCTTCTTAAGAGACTTCTGCGCGGCGGCTGCGCTGCC 157
Oy 61 GTCTCCAGACCGCGGCTGCGCGGCTGAGAGGATCAAACTGCTGCTGAGGTCAGCAT 120
Dh 158 GTCTCCAGACCGCGGCTGCGCGGCTGAGAGGATCAAACTGCTGCTGAGGTCAGCAT 217
Oy 121 GCCAGCAACAGATCACTGCTGAGAGCACTACAAAGCATATTGATGCTGTGTGAGA 180
Dh 218 GCCAGCAACAGATCACTGCTGAGAGCACTACAAAGCATATTGATGCTGTGTGAGA 277

Oy 181 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTGAGAGGGATTAACCTGGCCAAAGTCCT 240
Dh 278 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTGAGAGGGATTAACCTGGCCAAAGTCCT 337
Oy 241 TACTTCCCAACCAACCTCTCAACTTGGCTTCAAGAGAGATACAGAGCTCTTCTTA 300
Dh 338 TACTTCCCAACCAACCTCTCAACTTGGCTTCAAGAGAGATACAGAGCTCTTCTTA 397
Oy 301 GGGGCTGTGGATCGCATAGACAGTTCTGGCCCTACTTTGCTGCTGAACCTGGCGCT 360
Dh 398 GAGGCTGTGGATCGCATAGACAGTTCTGGCCCTACTTTGCTGCTGAACCTGGCGCT 457
Oy 361 GGGGCGGCTGGGCGGCAACCTCTCTCTCTCTGAGAGGGCTTACCAAGCTTCTGAGACAG 420
Dh 458 GGGGCGGCTGGGCGGCAACCTCTCTCTCTCTGAGAGGGCTTACCAAGCTTCTGAGACAG 517
Oy 421 TTGGCTGTGATGTGGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 477
Dh 518 TTGGCTGTGATGTGGGCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 577
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Dh 877 AGCATGCGCAAGACGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 922

FEATURES

source

Location/Qualifiers

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/db_xref="taxon:9606"

/clone="CSDDL011YJ23"

/clone_1ib="LTI_NFL010_BC2"

/sex="male"

/tissue_type="B cells from Burkitt lymphoma"

/contact="Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

1..909

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="CSDDL011YJ23"

/clone_1ib="LTI_NFL010_BC2"

/sex="male"

/tissue_type="B cells from Burkitt lymphoma"

/note="vector: pCMVSPORT 6; site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetechn.com URL : <http://fulllength.invitrogen.com>"

BASE COUNT 183 a 237 c 287 g 198 t 4 others

ORIGIN

Query Match 80.1%; Score 715.8; DB 9; Length 909;
Best Local Similarity 96.5%; Pred. No. 2.2e-189;
Matches 793; Conservative 3; Mismatches 16; Indels 10; Gaps 6;

OY 1 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCTGCGCGCGCGGTCGCCCTGCC 60
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DB 90 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCTGCGCGCGCGGTCGCCCTGCC 149
61 GTCTCCAGAGCCGGGTCGCCCATCGAG---AGGCTCAACTCTGCTGCAGGTCCA 116
|||||
DB 150 GTCTCCAGAGCCGGGTCGCCCATCGAGAAAGAAAGGAACTGCTGCTGCAGGTCCA 209
117 GCATGCCAGCAACAGATCAGTGGTGAAGACGATACAAAGGATCATGTATGTGTGT 176
|||||
DB 210 GCATGCCAGCAACAGATCAGTGGTGAAGACGATACAAAGGATCATGTATGTGTGT 269
177 GAGAACTCCCTAAGAGCAGGCGCTTCTCTTCTGAGAGGGGTAACTGGCCAAAGTAT 236
|||||
DB 270 GAGAACTCCCTAAGAGCAGGCGCTTCTCTTCTGAGAGGGGTAACTGGCCAAAGTAT 329
237 CCGTTACTTCCCAACCCAGCTCTCAACTTGCCTTCAAGAGCAAGTACAGACGCTCTT 296
|||||
DB 330 CCGTTACTTCCCAACCCAGCTCTCAACTTGCCTTCAAGAGCAAGTACAGACGCTCTT 389
297 CTTAGGGGCTGTGATGGCGATTAAGCACTTGGCGCTACTTGTGTGTAACCTGGCTC 356
|||||
DB 390 CTTAGGGGCTGTGATGGCGATTAAGCACTTGGCGCTACTTGTGTGTAACCTGGCTC 449
357 CGGTGGGCGCGCTGGGCGCACCTCCCTTGTCTTGTCTACCCGCGGACTTGTCTAGAC 416
|||||
DB 450 CGGTGGGCGCGCTGGGCGCACCTCCCTTGTCTTGTCTTGTCTACCCGCGGACTTGTCTAGAC 509
417 CAGGTGGCTGTGATGTGGCAGGCGCGC--CCAGCGTGAAGTTC-ATGCTCTGGGCGCA 473
|||||
DB 510 CAGGTGGCTGTGATGTGGCAGGCGCGC--CCAGCGTGAAGTTC-ATGCTCTGGGCGCA 569
474 CTGTATCATCAAGATCTTCAAGTCTGATGGCGCTGAGGGGCTCTACCAAGGCTTTCACAT 533
|||||
DB 570 CTGTATCATCAAGATCTTCAAGTCTGATGGCGCTGAGGGGCTCTACCAAGGCTTTCACAT 629
534 CTCTGTCCAGAGCATATTATCTATAGAGTGCCTACTTGCAGTCTGTATGATCTGCCCA 593
|||||
DB 630 CTCTGTCCAGAGCATATTATCTATAGAGTGCCTACTTGCAGTCTGTATGATCTGCCCA 688
594 -GGGAGTCTCTGACCCCAAGAAAGTGCACATTTTGTGAGCTGTGATTTGCCGAGA 652
689 GGGGAGTCTCTGACCCCAAGAAAGTGCACATTTTGTGAGCTGTGATTTGCCGAGA 748
653 GTGTGAGGAGTGTGGAGGCGTGTCTACCCCTTGTGACATGTTGCTGTGTAAGAAAGA 712
749 GTGTGAGGAGTGTGGAGGCGTGTCTACCCCTTGTGACATGTTGCTGTGTAAGAAAGA 808
713 TGATGCACTCCGCGGAGAAAGGCGGATATTATGTATACAGGGGACATTTGACTCTGGA 772
809 TGATGCACTCCGCGGAGAAAGGCGGATATTATGTATACAGGGGACATTTGACTCTGGA 868
773 GGAAGATTGCAAAAGAGAGAGGCAAGGCTTCTTCAAG 814
869 GGAAGATTGCAAAAGAGAGAGGCAAGGCTTCTTCAAGG 909

RESULT 6
BM466452 1043 bp mRNA linear EST 05-FEB-2002
LOCUS
DEFINITION
AGENCOURT_6431691 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5503575
5', mRNA sequence.
ACCESSION
BM466452
KEYWORDS
BM466452.1 GI:18515494
EST.

ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
NIH-MGC http://mgc.ncl.nih.gov/
1 (bases 1 to 1043)
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: LLM12143 row: 1 column: 16
High quality sequence stop: 744.

FEATURES
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Location/Qualifiers
1..1043
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_id="NIH_MGC_67"
/clone_id="NIH_MGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Average insert size 1.75 kb. Library constructed by Life
Technologies."

BASE COUNT 204 a 295 c 309 g 234 t 1 others

ORIGIN

Query Match 79.7%; Score 712.4; DB 13; Length 1043;
Best Local Similarity 97.8%; Pred. No. 2e-188;
Matches 744; Conservative 0; Mismatches 12; Indels 5; Gaps 2;

OY 1 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCTGCGCGCGCGGTCGCCCTGCC 60
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DB 91 ATGGGTGATCAGCGTTGGACCTTCTTAAGGACTTCTGCGCGCGCGGTCGCCCTGCC 150
61 GTCTCCAGAGCCGGGTCGCCCATCGAGAGGGTCAAACTGCTGCTGCAGAGTCCAGCAT 120
|||||
DB 151 GTCTCCAGAGCCGGGTCGCCCATCGAGAGGGTCAAACTGCTGCTGCAGAGTCCAGCAT 210
121 GCCAGCAACAGATCAGTCTGAGAAACAGTACAAAGGATCATTTGATGTGTGTGAGA 180
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DB 211 GCCAGCAACAGATCAGTCTGAGAAACAGTACAAAGGATCATTTGATGTGTGTGAGA 270
181 ATCCCTAAGAGCAGGCGCTTCTCTCTTCTGAGAGGGGTAACTGGCCAAAGTATCCGT 240
271 ATCCCTAAGAGCAGGCGCTTCTCTCTTCTGAGAGGGGTAACTGGCCAAAGTATCCGT 330
241 TACTTCCCAACCAAGCTCTCACTTGCCTTCAAGAGCAAGTACAGAGCTCTTCTTA 300
|||||
DB 331 TACTTCCCAACCAAGCTCTCACTTGCCTTCAAGAGCAAGTACAGAGCTCTTCTTA 390
301 GGGGCTGTGATTCGGCAATAGCACTTGTGGCGCTACTTGTGTATACCTGGGCTCCGGT 360
|||||
DB 391 GGGGCTGTGATTCGGCAATAGCACTTGTGGCGCTACTTGTGTATACCTGGGCTCCGGT 450
361 GGGGCTGTGATTCGGCAATAGCACTTGTGGCGCTACTTGTGTATACCTGGGCTCCGGT 420
|||||

Db 451 GGGGCGGCGGGCCACCCCTTGTCTTGTCTACCCCGCTGACTTGTGACACAG 510

Oy 421 TTGGCTGCTGATGTGGCAGCGC---CGCCAGCGCTGACTTCCATGCTGTGGCGACTGT 477

Db 511 TTTGGCTGCTGATGTGGCAGCGCGCCCGCCAGCGCTGACTTCCATGCTGTGGCGACTGT 570

Oy 478 ATCATCAAGATCTTCAAGCTGTGATGGCGCTGAGAGGGGCTCTACACAGGTTTCCAGCTCTCT 537

Db 571 ATCATCAAGATCTTCAAGCTGTGATGGCGCTGAGAGGGGCTCTACACAGGTTTCCAGCTCTCT 630

Oy 538 GTCCAAGGATCATTTATATAGAGCTGCTACTTCTGAGTCTATGATTAAGTCCAGAGG 597

Db 631 GTCCAAGGATCATTTATATAGAGCTGCTACTTCTGAGTCTATGATTAAGTCCAGAGG 690

Oy 598 ATGCTGCTGACCCCAAGACCTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 657

Db 691 ATGCTGCTGACCCCAAGACCTGCACATTTTGTGAGCTGATGATTTGCCAGAGTGTG 750

Oy 658 AGGAGATGCGAGGGCTGCTGTCTACCCCTTGTGACACTGCTGCTGATGATGATGATG 717

Db 751 AGGAGATGCGAGGGCTGCTGTCTACCCCTTGTGACACTGCTGCTGATGATGATGATG 810

Oy 718 CAGTCCGCGCGG--AAAGGGCCGATATTATGTACAGCGGG 756

Db 811 CAGTCCGCGCGCGAAGAGGGCCCATATTATGTACCGGGG 851

RESULT 7 990 bp mRNA linear EST 05-SEP-2001
LOCUS B1545249 603187373f1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:5258778 5',
DEFINITION mRNA sequence.
ACCESSION B1545249
VERSION B1545249.1 GI:15432561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:
AUTHORS Mammalia: Eutheria: Primates: Catarrhini: Homiidae: Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palokovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM11652 row: a column: 19
High quality sequence stop: 760.

FEATURES
source Location/Qualifiers
1..990

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5258778"
/clone_lib="NIH_MGC_95"
/issue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: Brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcagag
); Oligo-dr primed using primer 5'-TTTGTGTGTGTGTGTGT-3',
size-selected for average insert size 2.5 kb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT

191 a 262 c 320 g 217 t

ORIGIN

Query Match 79.4%; Score 709.6; DB 13; Length 990;
Best Local Similarity 93.4%; Pred. No. 1.2e-187;
Matches 818; Conservative 0; Mismatches 49; Indels 9; Gaps 7;

Oy 1 ATGGGTGATTCACCGCTTGAGGCTTCCATAAGACATTCGCGGCGGGGCGGTGCGCGTCC 60

Db 113 ATGGGTGATTCACCGCTTGAGGCTTCCATAAGACATTCGCGGCGGGGCGGTGCGCGTCC 172

Oy 61 GTCTCCAGAGCCGCGGCTGCGCCCATTCGAGAGGGCTCAAACTGCTCTGCTCAGTCCAGCAT 120

Db 173 GTCTCCAGAGCCGCGGCTGCGCCCATTCGAGAGGGCTCAAACTGCTCTGCTCAGTCCAGCAT 232

Oy 121 GCCAGCAAAAGATCAGTGTGAGAGGAGTCAAAAGGATCATTTGTTGTGTGAGA 180

Db 223 GCCAGCAAAAGATCAGTGTGAGAGGAGTCAAAAGGATCATTTGTTGTGTGAGA 292

Oy 181 ATCCCTAAGAGAGCAGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240

Db 293 ATCCCTAAGAGAGCAGGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 352

Oy 241 TACTTCCCCACCCCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTCTTCTTA 300

Db 353 TACTTCCCCACCCCAAGCTCTCAACTTCCCTTCAAGAGCAAGTACAGACAGCTCTTCTTA 412

Oy 301 GCGGCTGTGATCGGCATTAAGACAGTCTTGGCGCTACTTTCGTGTAACCTGCGTCCGCT 360

Db 413 GCGGCTGTGATCGGCATTAAGACAGTCTTGGCGCTACTTTCGTGTAACCTGCGTCCGCT 472

Oy 361 GCGGCTGTGAGGCGCACCTCCCTTGTGCTGCTACCGCGCTGAGTCTGCTGAGACAGG 420

Db 473 GCGGCTGTGAGGCGCACCTCCCTTGTGCTGCTACCGCGCTGAGTCTGCTGAGACAGG 532

Oy 421 TTGGCTGCTGATGTGGCAGCGC--CGCCAGCGCTGAGTTCATGCTGTGGCGCACTGTA 478

Db 533 TTGGCTGCTGATGTGGCAGCGCGCGCCAGCGCTGAGTTCATGCTGTGGCGCACTGTA 592

Oy 479 TCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGGCGCTTACCAGGTTTCAACGCTCTG 538

Db 593 TCATCAAGATCTTCAAGTCTGATGCGCTGAGAGGGCGCTTACCAGGTTTCAACGCTCTG 652

Oy 539 TCCAA-GGCATCATTTATCTATAGACCTGCTACCTGCGAGTCTATGATACGCCAAGGG 597

Db 653 TCCAAAGGATCATTTATCTATAGACCTGCTACCTGCGAGTCTATGATACGCCAAGGG 712

Oy 598 ATGCTGCTGTA-CCCCAAGAGCTGACATTTTGTG-AGCTGATGATTTGCCAGAGTG 655

Db 713 ATGCTGCTGTAAGCCCAAGAGCTGACATTTTGTGAGAGCTGATTTGCCAGAGTG 772

Oy 656 TGACGGCAGTGCAGAGGCTGCTG-TCCTAACCCCTTTCACACTGTTCTGCTGTAAGATGATG 714

Db 773 TGACGGCAGTGCAGAGGCTGCTGCTTCCACCTTTCGACACTGTTCTGCTGTAAGATGATG 832

Oy 715 ATGCAAGTCCGCGCGGAAGGGCGCATTTATGTAACAGGGGA-CAGTTGACTGCTGAG 773

Db 833 ATTCATTCGCGCGCGGAAGGGCGCATTTATGTAACAGGGGAAGAGTGAAGTCTGAG 892

Oy 774 GAAGATTTCAAAAG 833

Db 893 GAAGATTTGAG 950

Oy 834 GAGAGCATTTGGCGGCTGCTTTGTATTTGCTGTTGTA 869

Db 951 GAGAGCATTTGGCGGCGCGGAAGAGATGAGGCTGTGAA 986

RESULT 8 1033 bp mRNA linear EST 14-AUG-2001
LOCUS B1408731 602965692f1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5121071 5',
DEFINITION mRNA sequence.
ACCESSION B1408731

VERSION	BI408731.1	GI:15169654
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Eutheria; Rodentia; Sclirognathi; Muridae; Murinae; Mus	
AUTHORS	1 (bases 1 to 1033)	
TITLE	NIH-MGC http://mgc.nci.nih.gov/ .	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)	
COMMENT	Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	

Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
 Plate: LLM11295 row: 9 column: 24
 High quality sequence start: 5
 High quality sequence stop: 917.

FEATURES
Source

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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="5121071"
/clone_id="NC1_GCAP_Lu33"
/tissue_type="Pooled lung tumors"
/lab_host="DJ10B (phage-resistant)"
/notes="Organ: Lung; Vector: pPT73-Pac (Pharmacia) with a modified polylinker. Site_1: NotI; Site_2: EcoRI; 1st strand cDNA was prepared from mRNA obtained from pooled lung tumors with a Not I - oligo(dT) primer [5'-TGTTGACATCTGAAATGTCGCGCCGCTCTCTTTTCTTTTTT 3']."
/Pharmacia_stranded_cDNA_was_ligated_to_EcoRI_adaptors (Pharmacia), digested with Not I and cloned into the NotI and Eco RI sites of the modified pT73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. "

```

BASE COUNT	217 a	267 c	310 g	239 e
ORIGIN				

Query Match	78.0%;	Score 697.2;	DB 13;	Length 1033;
Best Local Similarity	88.0%;	Pred. No. 3.7e-184;		
Matches 783; Conservative	0;	Mismatches 103;	Indels 4;	Gaps 2;

QY	ATGGGGGATCAGCGCTTGGAGCTTCCCTAAAGAGATTTCTGGCCGGGGCGGTGGCGCTGCG	60
QY		
QY	76 ATCGGGGATCAGCGCTTGAAGCTTTCTTAAAGACTTCTGCGAGGTGGCATGCGCGCCGCC	135
QY	61 GTCTCCAAAGACCGCGGTGCGCCGCCCATCGAGAGGGTCAAACTGCTGCTGCAGTTCACAT	120
QY		
QY	136 GTCTCCAAAGACCGCGGTGCGCCGCCCATCGAGAGGGTCAAACTGCTGCTGCAGTTCACAT	195
QY	121 GCCAGCAAAAGATCAGTCTGTGAGAGCAGTACAAAGGATCTATTGATTTGTGTGTGAGA	180
QY		
QY	196 GCCAGCAAAAGATCAGTCTGTGAGAGCAAGTACAAAGGATCTATTGATTTGTGTGTGAGA	255
QY	181 ATTCCTAAAGAGAGGGCTTCTCTCTCTTCTGTGAGGGGTAACTGGCCAAAGTATCTCGT	240
QY		
QY	256 ATTCCTAAAGAGAGGGCTTCTCTCTCTTCTGTGAGGGGTAACTGGCCAAAGTATCTCGG	315
QY	241 TACTTCCCAACCAAGCTCTCAACTTCGCGCTTAAAGAGCAAGTAAAGCAAGCTCTCTTA	300
QY		
QY	316 TACTTCCCAACCAAGCTCTCAAGCTTCGCGCTTAAAGCAAGTAAAGCAAGTATCTCTG	375
QY	301 GGGGCGTGTGGATCGCATAAAGCAAGTCTGGCGCTACTTCTGTGTAACTGGCGTCCGGT	360
QY		
QY	376 GGAGGCGTGTGGATCGCATAAAGCAAGTCTGGCGCTACTTCTGTGTAACTGGCGTCTGGT	435

OY	361	GGGGCCGGTGGGGGCACCTCCCTTGGCTTTGATACCGCGTGGACTTGGTAGGACAGG	420
Db	436	GGGGCAGCTGGGGCCACCTCCCTTGCTTGCTATCCCGCTGGACTTGGTAGGACAGG	495
OY	421	TTGGCTGCTGATGTGGGGAGGCG---GGCCAGCGTGAGTTGCATGGTCTGGGAGACTGT	477
Db	496	CTGGCTGCCGACGTGGGCGAAGGAGATCTTCCAGCGAGAAATTCAATGGGCTGGGAGACTGT	555
OY	478	ATCATCAAGATCTTCAAGCTGTGATGGCTGAAGGGGCTCTACAGGGCTTTCACGCTCTCT	537
Db	556	CTCACCAAGATCTTCAAGTCCGAGCGGCTGAAGGOTCTACCAAGGGTTTCAGTGTCTCT	615
OY	538	GTCCAGGCGATCATTTATCTATAGAGCTGCCACTTTCGGAGTCTATGATACTGCCAAGGGG	597
Db	616	GTCCAGGCGATCATCATCTACAGAGGCTGCCACTTTCGGAGTCTATGACACACGCCAAGGGG	675
OY	598	ATGCTCCCTGACCCCAAGCAGTCACATTTTGTGACCTGGATGATTTGGCCAGAGTGG	657
Db	676	ATGCTGCCAGACCCCAAGAAATGTGCACATTTATCGAGCTGGATGATTTGCCAGAGTGG	735
OY	658	ACGGCAGTCG--CAGGCGTGTCTGTCTTACCCTTTTGACACTTTCGTCTGTAGAAATGATAT	716
Db	736	ACAGCGGTGGCGGGGGCTGTGTCTCTATACGCTTGTTGACACTTTCGTCTAGAGATGATAT	795
OY	717	GCAGTCCGCCCGGAAGAGGGCGCGATATTATGTACACGGGAGCAGTTGACTCTGTGAGGAA	776
Db	796	GCAGTCTGCCCGGAAGAGGGCGCGATATTATGTACACGGGAGCAGTTGACTCTGTGAGGAA	855
OY	777	GATTGCAAAACGACGAGGACCGAAGGCTTCTTCAAGGTGCTGTGTCATATGTCTGAG	836
Db	856	GATTGCCAAAGATGAGAGGACCAACGCTTCTTCAAGGCTCTTGCTCAATGTACTGAG	915
OY	837	AGGCATGGCGGCTCTTTGTATTGGTGTTCATATGATGAGATCAAAATAANT	886
Db	916	AGCGCTTGTGGTGTCTTTGATGGCGATGATGATGATGATCAAAACT	965

RESULT 9	
B1458368	
LOCUS	879 bp mRNA linear EST_21-Aug-2001
DEFINITION	603198738P1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:5278233 5',
ACCESSION	mRNA Sequence.
VERSION	B1458368 B1458368 .1 GI:15249024

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 879)	NIH-MGC http://mgc.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)	Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Mikiros Paltovits, M.D., Ph.D.
 cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraak
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MCC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM11702 row: 1 column: 10
 High quality sequence stop: 776.

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FEATURES
source
location/Qualifiers
1..879
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/db_xref="taxon:9606"
/clone="IMAGE:5278233"
/clone_11b="NH-MCC-96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
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/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site.1: BamHI; Site.2: SalI-XhoI (gtcgaag) : Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTAA-3', size selected for average insert size 2.3 kb and normalized to 10⁶ copies. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 175 a 234 c 267 g 203 t
ORIGIN

Query Match 76.2%: Score 681.2; DB 13; Length 879;
Best Local Similarity 96.5%: Pred. No. 1e-179;
Matches 762: Conservative 0; Mismatches 18; Indels 10; Gaps 6;

OY 1 ATGGGTCATCAGCTTGGAGCTTCTAAAGAGCTCTGCGCGGGCGTCCGCGTCC 60
DB 60 ATGAGTATCAGCTTGGAGCTTCTAAAGAGCTCTGCGCGGGCGTCCGCGTCC 119
OY 61 GTCTCCAAAGACCGCGTCCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCC 120
DB 120 GTCTCCAAAGACCGCGTCCGCGCGTCCGCGTCCGCGTCCGCGTCCGCGTCC 179
OY 121 GCCAGCAAGAGATCAGTCTGAGAGAGAGTACAAAGGAGTATGCTGCTGAGAG 180
DB 180 GC---CAACACAGTCACTGCTGAGAACCACTACAAAGGATGATGCTGCTGAGAG 236
OY 181 ATCCCTAAGAGAGAGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 237 ATCCCTAAGAGAGAGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 296
OY 241 TACTTCCCAAGAGAGAGTCTCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 297 TACTTCCCAAGAGAGAGTCTCAAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCT 356
OY 301 GGGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 360
DB 357 GGGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 416
OY 361 GGGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 417 GGGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 476
OY 421 TTGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 477
DB 477 TTGGCTGTGATGGGCTAAGAGAGTCTGCGCTGCTGCTGCTGCTGCTGCTGCT 536
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DB 597 GTCCAAGAGATCTTCAAGTCTGAGAGAGAGGCTTCAAGAGAGGCTTCAAGAG 656
OY 597 GATGCTGTGAG 655
DB 657 GATGCTGTGAG 716
OY 656 TGACGAGTGTGAG 715
DB 717 TGACGAGTGTGAG 775
OY 716 TGACGAGTGTGAG 775
DB 776 TGACGAGTGTGAG 834
OY 776 AGATTGCAAA 785
DB 835 AGATTGCAAA 844

RESULT 10
BM459526
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM459526 882 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6417828 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:534143
5', mRNA sequence.
BM459526
BM459526.1 GI:18508566
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 882)
NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-femail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
plate: LLAM12220 row: c column: 08
high quality sequence stop: 731.
Location/Qualifiers
1. 882
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:534143"
/clone_1ib="NIH_MGC_71"
/issue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-Sport6; Site.1: NotI;
Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb."
BASE COUNT 204 a 208 c 241 g 229 t
ORIGIN

Query Match 75.7%: Score 676.6; DB 13; Length 882;
Best Local Similarity 99.0%: Pred. No. 2e-178;
Matches 692: Conservative 0; Mismatches 4; Indels 3; Gaps 1;

OY 199 TTCTCTCTCTCTGAGAGGCTAAGCTGAGCAAGTATCGTACTTCCCAAGAGCT 258
DB 2 TTCTCTCTCTCTGAGAGGCTAAGCTGAGCAAGTATCGTACTTCCCAAGAGCT 61
OY 259 CTCACCTTGGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 318
DB 62 CTCACCTTGGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 121
OY 319 AACGATTTGGGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 378
DB 122 AACGATTTGGGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAG 181
OY 379 TCCCTTGTGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 438
DB 182 TCCCTTGTGCTTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 241
OY 439 AGGCG---CGCCAGGCTGAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
DB 242 AAGGCGCGCCAGGCTGAGTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
OY 496 TCGATGAGCTGAGAGAGAGTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAG 555
DB 302 TCGATGAGCTGAGAGAGAGTCAAGAGAGAGTCAAGAGAGAGAGAGAGAGAGAG 361
OY 556 TATAGAGTGTCTACTTGTGAGAGTATGATGATGATGATGATGATGATGATGAT 615
DB 362 TATAGAGTGTCTACTTGTGAGAGTATGATGATGATGATGATGATGATGATGAT 421

QY	616	AACGTGCACATTTTGTGAGCTGGATGATTTGCCAGATGTGACGGGACGTGGCAGGGCTG	675
Db	422	AACGTGCACATTTTGTGAGCTGGATGATTTGCCAGATGTGACGGGACGTGGCAGGGCTG	481
QY	676	CTGTCTCAACCCCTTGGACACTGTTCTGCTGTAAGATGATGATGACATCCGGCGGCAAAAGG	735
Db	482	GTGTCTCAACCCCTTGGACACTGTTCTGCTGTAAGATGATGATGACATCCGGCGGCAAAAGG	541
QY	736	GCCGATATTATGTACAGGGGACAGTTGACTGTGGAGAGAGATTGCCAAAAGACAAAGCA	795
Db	542	GCCGATATTATGTACAGGGGACAGTTGACTGTGGAGAGAGATTGCCAAAAGACAAAGCA	601
QY	796	GCCAAAGCCCTTCTTCAAAAGCTGCCCTGATGCCAATGTGCTGAGAGGCATGGCGGCTCTTT	855
Db	602	GCCAAAGCCCTTCTTCAAAAGCTGCCCTGATGCCAATGTGCTGAGAGGCATGGCGGCTCTTT	661
QY	856	GTAATGCTGTCTATGATGAGATGCAAAAAAATATGTCTTAA	894
Db	662	GTAATGCTGTCTATGATGAGATGCAAAAAAATATGTCTTAA	700

RESULT 11
BI667026
LOCUS 907 bp mRNA linear EST 12-Sep-2001
DEFINITION 603291895F1 NIH_MGC_96 Homo sapiens CDNA clone IMAGE:531319 5',
mRNA sequence.
ACCESSION BI667026
VERSION BI667026
KEYWORDS GI:15581259
SOURCE EST.
ORGANISM human.
human sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 907)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgap@remail.ru.nl
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA library preparation: Michael J. Brownstein (NHGRI), Shihaki
Toshiyuki and Piero Carninci (RIKEN)
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNMI178 row: n column: 24
High quality sequence stop: 806.

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FEATURES
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    location/Qualifiers
      1. 907
        /organism="Homo sapiens"
        /db_xref="taxon:9606"
        /clone="IMAGE:5111319"
        /clone_1lb="NIH_MGC_96"
        /tissue_type="hypothalamus"
        /lab_host="DH10B"
        /note="Organ: brain; Vector: pBluescript (modified
        pBluescript KS+); Site.1: BamHI; Site.2: SalI; XhoI (gtcga
        ) ; Oligo-dt primed using primer 5'-TTTTTTTTTTTTTTTT-3',
        size selected for average insert size 2.3 kb and
        normalized to ROT 5. This is a primary library enriched
        for full-length clones and constructed using the
        CAP-trapper method (Carninci, in preparation). Library
        constructed by M. Brownstein (NIH/NHGRI, National
        Institutes of Health). Note: this is a NIH_MGC library."
BASE COUNT
ORIGIN
  174 a
    253 c      287 g      193 t

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Query Match	75.08;	Score 670.4;	DB 13;	Length 907;
Best Local Similarity	97.18;	Pred. NO. 1.1e-176;		
Matches 726; Conservative	0;	Mismatches 16;	Indels 6;	Gaps 4

Oy	1	ATGGGTATATCAGCGTTTGAGACTTCTCTAAAGACATCTCTGGCCGGGGCGGTGCGCGCTGCC	60
Db	113	ATGGGGTATCAGCGTTTGAGACTTCTCTAAAGACATCTCTGGCCGGGGCGGTGCGCGCTGCC	172
Oy	61	GTCACCAAGACCGCGGTGCGCCCATATGAGAGGCTCAAACTGCTGTACAGTCCACAT	120
Db	173	GTCACCAAGACCGCGGTGCGCCCATATGAGAGGCTCAAACTGCTGTACAGTCCACAT	232
Oy	121	GCCAGCAAAACAGATCAGTGTCTGAGAACAGTATCAAAAGGATCATTTGATTTGTGTGTAGA	180
Db	233	GCCAGCAAAACAGATCAGTGTCTGAGAACAGTATCAAAAGGATCATTTGATTTGTGTGTAGA	292
Oy	181	ATCCCTAAGAGACAGGGCTTCTCTGCTTCTGTGAGGGGTAACTCTGGCCAAAGTATCCGT	240
Db	293	ATCCCTAAGAGACAGGGCTTCTCTGCTTCTGTGAGGGGTAACTCTGGCCAAAGTATCCGT	352
Oy	241	TACTTTCCACCACCAAGCTCTCACTTCCCTTCAAGAGCAAGTACMAAGCAGCTCTTTCTTA	300
Db	353	TACTTTCCACCACCAAGCTCTCACTTCCCTTCAAGAGCAAGTACMAAGCAGCTCTTTCTTA	412
Oy	301	GGGGGTGTGATCGGCATTAACAGATTTCTGGCGCTACTTTGCTGTCTAACCTGGCGCCGT	360
Db	413	GGGGGTGTGATCGGCATTAACAGATTTCTGGCGCTACTTTGCTGTCTAACCTGGCGCCGT	472
Oy	361	GGGGGCGGTGGGGGCCACCTCCCTTTGCTGTACCCGCTGAGACTTTGCTAGACACAG	420
Db	473	GGGGGCGGTGGGGGCCACCTCCCTTTGCTGTACCCGCTGAGACTTTGCTAGACACAG	532
Oy	421	TTGGCTGTGATGTGGGCGACGCG---CGCCACAGCGTGAATTTCATGTCTGTGGCGAGTGT	477
Db	533	TTGGCTGTGATGTGGGCGACGCGCGCCACAGCGTGAATTTCATGTCTGTGGCGAGTGT	592
Oy	478	ATCATCAAGATCTTCAAGTCTGTATGGGCTGAGGGGGCTCTACAGGGTTTCAAGCTCTCT	537
Db	593	ATCATCAAGATCTTCAAGTCTGTATGGGCTGAGGGGGCTCTACAGAGGTTTCAAGCTCTCT	652
Oy	538	GTCCAAAGCATCATTTATCTATAGAGCTGCTACCTCGGAGTCTATGATACACTGCAAGGGG	597
Db	653	GTCCAAAGCATCATTTATCTATAGAGCTGCTACCTCGGAGTCTATGATACACTGCAAGGGG	712
Oy	598	ATGCTGCTGACCCCAAGACAGTGCACATTTTGTGTAGCT--GGATGATTTGCCACAGTGT	656
Db	713	ATGCTGCTGAC--CCCAAGACAGTGCACATTTTGTGTAGCTGAGATTTGCCACAGTGT	771
Oy	657	GACGGCAGTTCGAGGGCT--GCTGTCTTACCCCTTTGACACTGTTGCTGTAGATGATGAGA	715
Db	772	GACCCACAGTCGAGGGGCTGTGGTGTCTACCCCTTTTGTGACACTGTTGCGCCTAAATAGTGA	831
Oy	716	TGCAGTCCGCGGAAAGGGCGCGATAT 743	
Db	832	TGCCGCCCGCGGAAAGGGCGCGCATAT 859	

RESULT 12
BO214399
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BO214399 862 bp mRNA linear EST 02-MAY-2002
AGENCOURT_7553137 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:5058078
5', mRNA sequence.
BO214399
BO214399.1 GI:20395799
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 862)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF/Gazdar
cDNA library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13322 row: 1 column: 23
High quality sequence stop: 708.

FEATURES

SOURCE

1..862
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6058078"
/clone_lib="NIH MGC 68"
/tissue_type="large cell carcinoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 162 a 232 c 272 g 194 t 2 others

ORIGIN

Query Match

Best Local Similarity 98.1%; Score 665.8; DB 14; Length 862;
Matches 706; Conservative 0; Mismatches 8; Indels 6; Gaps 3;

OY 1 ATGGGATACACCTTGGAGCTTCTTAAGACCTCTCGCGCGGCGGCTGCC 60
DB 97 ATGGGTATACCTTGGAGCTTCTTAAGACCTCTCGCGCGGCGGCTGCC 156
OY 61 GTCTCCAAAGACCGGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
DB 157 GTCTCCAAAGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 216
OY 121 GCCAGCAACAGATCAGTGTGAGAGCACTACAAAGGATCATTTGTGTGAGA 180
DB 217 GCCAGCAACAGATCAGTGTGAGAGCACTACAAAGGATCATTTGTGTGAGA 276
OY 181 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 277 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 336
OY 241 TACTTCCCGCCAGCCTCTCAACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
DB 337 TACTTCCCGCCAGCCTCTCAACTTCTCTCTCTCTCTCTCTCTCTCTCTCT 396
OY 301 GGGGGTGTGATGAGGATTAAGAGAGTCTGCGGCTACTTGTCTGTAACCTGCGGCT 360
DB 397 GGGGGTGTGATGAGGATTAAGAGAGTCTGCGGCTACTTGTCTGTAACCTGCGGCT 456
OY 361 GGGGGCTGTGGGCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
DB 457 GGGGGCTGTGGGCGACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 516
OY 421 TTGGCTGTGATGTGGGCGAGGCG--CGGCCAGCGAGTCCATGCTGGCGGCACT 477
DB 517 TTGGCTGTGATGTGGGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 576
OY 478 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGGCGGCTTACCAAGGTTTCAAGCTCT 537
DB 577 ATCATCAAGATCTTCAAGTCTGATGCGCTGAGGCGGCTTACCAAGGTTTCAAGCTCT 636
OY 538 GTTCAAGGATCTTATTTATATAGAGTGGCTTCTGAGTGTATGATGCAAGGAG 597
DB 637 GTTCAAGGATCTTATTTATATAGAGTGGCTTCTGAGTGTATGATGCAAGGAG 696
OY 598 ATGCTGCTGACCCCAAGAAGCGTCAATTTTGTGAGTGGATGATTTCCCAAGCTGTG 657
DB 697 ATGCTGCTGACCCCAAGAAGCGTCAATTTTGTGAGTGGATGATTTCCCAAGCTGTG 756
OY 658 ACGGAGTGGCAGGCTGCT-GTCTTACCCCTTTTGAAGCTG--TTTGTGATGATGATG 714
DB 757 ACGGAGTGGCAGGCTGCTGCTTACCCCTTTTGAAGCTGATGCTGATGATGATG 816

RESULT 13

BI412906 888 bp mRNA linear EST 14-AUG-2003

LOCUS

602987149F1 NC1_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5143188 5',

DEFINITION

mRNA sequence.

ACCESSION

BI412906

VERSION

BI412906.1 GI:15173829

KEYWORDS

EST.

SOURCE

house mouse.

ORGANISM

Mus musculus

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

TITLE

NIH-MGC <http://imgc.ncbi.nlm.nih.gov/>.

JOURNAL

National Institutes of Health, Mammalian Gene Collection (MGC)

COMMENT

unpublished (1999)

CONTACT

Contact: Robert Strausberg, Ph.D.

EMAIL

Email: cgaps-f@mail.nih.gov

TISSUE

Tissue Procurement: Gilbert Smith, Ph.D.

PREPARATION

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima

CDNA

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA

DNA Sequencing by: Incyte Genomics, Inc.

CLONE

Clone distribution: NC1-CGAP clone distribution information can be

FOUND

found through the I.M.A.G.E. Consortium/LLNL at:

PLATE

<http://image.llnl.gov> Plate: LLAM1353 row: a column: 13

QUALITY

High quality sequence start: 15

SEQUENCE

High quality sequence stop: 878.

FEATURES

SOURCE

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Location/Qualifiers
/organism="Mus musculus"
/strain="C2BECH 11"
/db_xref="taxon:10090"
/clone="IMAGE:5143188"
/clone_lib="NC1-CGAP_Lu33"
/tissue_type="pooled lung tumors"
/lab_host="DH108 (phage-resistant)"
/note="Organ: lung; Vector: pTZ19-pac (Pharmacia) with a
modified polylinker. Site_1: NotI; Site_2: EcoRI; 1st
strand cDNA was prepared from mRNA obtained from pooled
lung tumors with a Not I - oligo(dT) primer [5']
TGTACCAATCTGAGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia). digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTZ19 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Fatima Bernaldo."

BASE COUNT 185 a 236 c 267 g 200 t

ORIGIN

Query Match

Best Local Similarity 90.0%; Score 664.2; DB 13; Length 888;
Matches 735; Conservative 0; Mismatches 78; Indels 4; Gaps 2;

OY 1 ATGGGATACACCTTGGAGCTTCTTAAGAGCTTCTCGCGGCGGCGGCTGCC 60
DB 62 ATGGGATACACCTTGGAGCTTCTTAAGAGCTTCTCGCGGCGGCGGCTGCC 121
OY 61 GTTCCAAAGACCGGCTGCGCCCATCGAGAGGCTCAAACTGCTGAGTCCAGCAT 120
DB 122 GTTCCAAAGACCGGCTGCGCCCATCGAGAGGCTCAAACTGCTGAGTCCAGCAT 181
OY 121 GCCAGCAACAGATCAGTGTGAGAGCACTACAAAGGATCATTTGTGTGAGA 180
DB 182 GCCAGCAACAGATCAGTGTGAGAGCACTACAAAGGATCATTTGTGTGAGA 241
OY 181 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240
DB 242 ATCCCTAAGAGAGGAGGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 301

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OY 241 TACTTCCCACCAAGCTCTCACTTGGCTTCAAGACAAGTACAGACAGCTCTTCTTA 300
    ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 302 TACTTCCCACCAAGCTCTCACTTGGCTTCAAGACAAGTACAGACAGCTCTTCTTA 361
OY 301 GGGGGTGTGATCGCATTAAGCAGTTCTGGCGCTACTTGTCTGTAACCTGGCGCT 360
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 362 GGAGCGGTGATCGCATTAAGCAGTTCTGGCGCTACTTGTCTGTAACCTGGCGCT 421
OY 361 GGGGGCGTGGGGCGGACCTGCTTGTCTGTAACCTGGCGCTACTTGTCTGTAAC 420
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 422 GGGGCGAGCTGGGGCGGACCTGCTTGTCTGTAACCTGGCGCTACTTGTCTGTA 481
OY 421 TTGGCTGCTGATGTGGGCGGCG---CGCCGACGCTGATGCTGTGGCGGACAGT 477
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 482 CTGGCTGCCGAGCTGGGCGGAGGATCTTCCAGCGAGATTCATATGGCTGGCGAG 541
OY 478 ATCATCAAGATCTTCAAGTGTGATGGCTGAGGGGCTCTACCGAGGTTTCACAG 537
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 542 CTCACCAAGATCTTCAAGTGTGATGGCTGAGGGGCTCTACCGAGGTTTCAGTCT 601
OY 538 GTCCAAAGCATCATATATCTATAGAGCTGCTACTTGGAGTCTATGATACCTGCA 597
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 602 GTCCAGGGCATCATATCTATAGAGCTGCTACTTGGAGTCTATGATACCTGCA 661
OY 598 ATGCTGCTGACCCCAAGACGCTGACATTTTGTGAGCTGATGATGGCCAGAGT 657
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 662 ATGCTGCTGACCCCAAGACGCTGACATTTTGTGAGCTGATGATGGCCAGAGT 721
OY 658 ACGGAGTGTGCAAGGGCTGCTGTCTACCCCTTGTGACGCTGTCTGATGATGAT 717
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 722 ACAGCGGTGTGGGGGCTGTGTCTATCTATCCGTTTGACACTGTTCGTAAGAT 781
OY 718 CAGTCCGCGCGGAAGGGGCGGATTTATGTAACAGGGGACAGTTGACTGCTGAG 777
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 782 CAGCTGTGCGGGAAGGGGCTGTATTTATGTAACAGGGGACAGTTGACTGCTG 841
OY 778 ATTGCAAAAGACAGAGGACCAAGGCTTCTTCAAG 814
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 842 ATTGC-AAAGATGAACGAGCCACGCTTCTTCAAG 877

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RESULT 14
LOCUS B1256359
DEFINITION 602975222F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5114621 5',
    mRNA sequence.
ACCESSION B1256359
VERSION B1256359.1 GI:14810692
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 948)
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
    Email: cga@bbs-remail.nih.gov
    Tissue Procurement: ATCC
    cDNA Library Preparation: Life Technologies, Inc.
    cDNA Library Arrayed by: Incyte Genomics, Inc.
    DNA Sequencing by: Incyte Genomics, Inc.
    Clone distribution: MGC clone distribution information can be
    found through the I.M.A.G.E. Consortium/LLNL at:
    http://image.llnl.gov
    Plate: LLAM11278 row: k column: 06
    High quality sequence stop: 789.
FEATURES
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            /db_xref="taxon:9606"
            /clone="IMAGE:5114621"

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BASE COUNT 193 a 233 c 315 g 207 t
ORIGIN
Query Match 74.2% Score 663; DB 13; Length 948;
Best Local Similarity 93.6%; Pred. No. 1.3e-174;
Matches 759; Conservative 0; Mismatches 40; Indels 12; Gaps 6;

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    /clone.lib="NIH_MGC_12"
    /tissue.type="cervical carcinoma cell line"
    /lab_host="DH10B"
    /note="Organ: cervix; Vector: pCMV-SPORT6; Site:1; Notcl:
    Site-2; Salt: Cloned unidirectionally. Primer: Oligo dT.
    Average insert size 1.4 kb. Library prepared by Life
    Technologies."
DB 96 ATGGGTATACACGCTTGGAGCTTCTTAAAGCATCTTCTGCGGGGCGGCTCCCGCTCC 155
OY 61 GTCTCAAGACCGGGGTGCGCCCATTCAGAGGGGTCAAACTGCTGCGAGGTCCAGCAT 120
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 156 GTCTCAAGACCGGGGTGCGCCCATTCAGAGGGGTCAAACTGCTGCGAGGTCCAGCAT 215
OY 121 GCCAGCAACAGATCAGTGTGAGAGCAGTACAAAGGATCATGATTGTGTGTGAGA 180
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 216 GCGACCAACAGATCAGTGTGAGAGCAGTACAAAGGATCATGATTGTGTGTGAGA 275
OY 181 ATCCCTAAGAGACAGGCTTCTCTCTCTTCTGTGAGGGGTAACTGCGCAACGTGAT 240
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 276 ATCCCTAAGAGAGAGGCTTCTCTCTCTTCTGTGAGGGGTAACTGCGCAACGTGAT 335
OY 241 TACTTCCCACCAAGCTCTCACTTGGCTTCAAGACAAGTACAGACAGCTCTTCTTA 300
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 302 TACTTCCCACCAAGCTCTCACTTGGCTTCAAGACAAGTACAGACAGCTCTTCTTA 361
OY 301 GGGGGTGTGATCGCATTAAGCAGTTCTGGCGCTACTTGTCTGTAACCTGGCGCT 360
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 362 GGAGCGGTGATCGCATTAAGCAGTTCTGGCGCTACTTGTCTGTAACCTGGCGCT 421
OY 361 GGGGGCGTGGGGCGGACCTGCTTGTCTGTAACCTGGCGCTACTTGTCTGTAAC 420
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 422 GGGGCGAGCTGGGGCGGACCTGCTTGTCTGTAACCTGGCGCTACTTGTCTGTA 481
OY 421 TTGGCTGCTGATGTGGGCGGCG---CGCCGACGCTGATGCTGTGGCGGACAGT 477
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 482 CTGGCTGCCGAGCTGGGCGGAGGATCTTCCAGCGAGATTCATATGGCTGGCGAG 541
OY 478 ATCATCAAGATCTTCAAGTGTGATGGCTGAGGGGCTCTACCGAGGTTTCACAG 537
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 542 CTCACCAAGATCTTCAAGTGTGATGGCTGAGGGGCTCTACCGAGGTTTCAGTCT 601
OY 538 GTCCAAAGCATCATATATCTATAGAGCTGCTACTTGGAGTCTATGATACCTGCA 597
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 602 GTCCAGGGCATCATATCTATAGAGCTGCTACTTGGAGTCTATGATACCTGCA 661
OY 598 ATGCTGCTGACCCCAAGACGCTGACATTTTGTGAGCTGATGATGGCCAGAGT 657
    ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 662 ATGCTGCTGACCCCAAGACGCTGACATTTTGTGAGCTGATGATGGCCAGAGT 721
OY 658 ACGGAGTGTGCAAGGGCTGCTGTCTACCCCTTGTGACGCTGTCTGATGATGAT 717
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 722 ACAGCGGTGTGGGGGCTGTGTCTATCTATCCGTTTGACACTGTTCGTAAGAT 781
OY 718 CAGTCCGCGCGGAAGGGGCGGATTTATGTAACAGGGGACAGTTGACTGCTGAG 777
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 782 CAGCTGTGCGGGAAGGGGCTGTATTTATGTAACAGGGGACAGTTGACTGCTG 841
OY 778 ATTGCAAAAGACAGAGGACCAAGGCTTCTTCAAG 814
    ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 842 ATTGC-AAAGATGAACGAGCCACGCTTCTTCAAG 877

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RESULT 15
B0947818

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